

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 18:14:26 ; Search time 134 Seconds  
(without alignments)  
116.836 Million cell updates/sec

Title: US-10-723-368-5

Perfect score: 254  
Sequence: 1 TQQLRVGCVLGTCTQVQNL.....MGPRGRQDSAPVDPSSPHSY 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapect 0.5

Searched: 1426032 seqs, 333106140 residues

Total number of hits satisfying chosen parameters: 1426032

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubppaa/PCR\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubppaa/PCRUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubppaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubppaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubppaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubppaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubppaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubppaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubppaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubppaa/US10E\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	254	100.0	47	US-10-850-055-14	Sequence 14, Appl
2	72.5	28.5	52	US-09-813-345-14	Sequence 14, Appl
3	72.5	28.5	52	US-10-197-954-2	Sequence 2, Appl
4	72.5	28.5	52	US-10-474-635A-19	Sequence 19, Appl
5	72.5	28.5	52	US-10-718-071-43	Sequence 43, Appl
6	72.5	28.5	52	US-10-760-085-2	Sequence 2, Appl
7	72.5	28.5	185	US-10-364-889-6	Sequence 6, Appl
8	72.5	28.5	185	US-10-372-683-12	Sequence 12, Appl
9	72.5	28.5	185	US-10-675-406A-7	Sequence 7, Appl
10	72.5	28.5	185	US-10-755-889-148	Sequence 148, Appl
11	69.5	27.0	50	US-09-813-345-15	Sequence 15, Appl
12	68.5	27.0	52	US-10-718-071-16	Sequence 16, Appl
13	64	25.2	103	US-10-264-237-1622	Sequence 1622, Ap

14	63.5	25.0	216	US-10-437-963-198108	Sequence 198108,
15	62.5	24.6	52	US-10-360-101-74	Sequence 74, Appl
16	59	23.2	142	US-10-307-817-14	Sequence 14, Appl
17	58.5	23.0	92	US-10-437-963-198935	Sequence 198935,
18	58.5	23.0	521	US-10-437-963-124602	Sequence 26, Appl
19	58.5	23.0	576	US-10-184-648-26	Sequence 8, Appl
20	58	22.8	560	US-10-238-129-8	Sequence 8, Appl
21	58	22.8	560	US-10-238-667-8	Sequence 6078, Ap
22	58	22.8	1544	US-10-369-493-6078	Sequence 6078, Ap
23	57	22.4	117	US-10-767-701-51114	Sequence 51114, A
24	56.5	22.2	575	US-10-425-114-64569	Sequence 64569, A
25	56	22.0	89	US-10-437-963-136207	Sequence 136207,
26	56	22.0	107	US-09-764-870-456	Sequence 356, App
27	56	22.0	107	US-09-764-853-470	Sequence 470, App
28	56	22.0	107	US-10-125-540-356	Sequence 356, App
29	56	22.0	107	US-10-103-313-301	Sequence 301, App
30	56	22.0	107	US-10-158-057-335	Sequence 335, App
31	56	22.0	947	US-10-461-194-114	Sequence 114, App
32	55	21.7	220	US-10-767-701-32051	Sequence 32051, A
33	55	21.7	322	US-10-424-599-175411	Sequence 175411,
34	55	21.7	669	US-10-120-801-108	Sequence 108, App
35	54.5	21.5	126	US-10-437-963-202043	Sequence 202043,
36	54.5	21.5	320	US-10-437-963-119917	Sequence 119917,
37	54.5	21.5	751	US-10-437-963-135754	Sequence 135754,
38	54	21.3	538	US-10-437-963-151317	Sequence 151317,
39	53.5	21.1	135	US-10-264-049-4093	Sequence 4093, Ap
40	53.5	21.1	303	US-10-097-340-143	Sequence 143, App
41	53.5	21.1	303	US-10-171-311-87	Sequence 87, Appl
42	53.5	21.1	329	US-09-999-121-6	Sequence 48541, A
43	53	20.9	86	US-09-864-761-48541	Sequence 48541, A
44	53	20.9	117	US-09-789-390-41	Sequence 41, Appl
45	53	20.9	136	US-10-156-761-8659	Sequence 8659, Ap

#### ALIGNMENTS

RESULT 1  
US-10-850-055-14  
: Sequence 14, Application US/10850055  
: Publication No. US2005009742A1  
: GENERAL INFORMATION:  
: APPLICANT: Bertilsson, Goran  
: APPLICANT: Erlanson, Rikard  
: APPLICANT: Fritsen, Jonas  
: APPLICANT: Haegerstrand, Anders  
: APPLICANT: Haedrich, Jessica  
: APPLICANT: Hellstrom, Kristina  
: APPLICANT: Hagbladh, Johan  
: APPLICANT: Jansson, Katarina  
: APPLICANT: Kortessan, Jarkko  
: APPLICANT: Lindquist, Per  
: APPLICANT: Lundh, Hanna  
: APPLICANT: McGuire, Jacqueline  
: APPLICANT: Mercer, Alex  
: APPLICANT: Nyberg, Karl  
: APPLICANT: Oseolnak, Amna  
: APPLICANT: Patrone, Cesare  
: APPLICANT: Ronholm, Harriet  
: APPLICANT: Wikstrom, Lillian  
: APPLICANT: Zachrisson, Olof  
: TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS  
: FILE REFERENCE: 21882-517 CIP  
: CURRENT APPLICATION NUMBER: US/10/850,055  
: CURRENT FILING DATE: 2004-05-19  
: PRIOR APPLICATION NUMBER: US 10/718,071  
: PRIOR FILING DATE: 2003-11-20  
: PRIOR APPLICATION NUMBER: US 60/427,912  
: PRIOR FILING DATE: 2002-11-20  
: NUMBER OF SEQ ID NOS: 66  
: SOFTWARE: PatentIn version 3.2  
: SEQ ID NO 14  
: LENGTH: 47

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-850-035-14

Query Match 100.0%; Score 254; DB 17; Length 47;  
Best Local Similarity 100.0%; Pred. No. 1.2e-25;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQQLRVGCVLTGTCOVONLSHRLMQLMGPAGQDSAPVDPSSPHSY 47  
DB 1 TQQLRVGCVLTGTCOVONLSHRLMQLMGPAGQDSAPVDPSSPHSY 47

## RESULT 2

US-09-813-345-14  
Sequence 14, Application US/09813345  
Patent No. US20020068814A1  
GENERAL INFORMATION:  
APPLICANT: Smith, Derek D.  
Saha, Shankar  
Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR  
SUPERFAMILY AND METHODS OF USE

NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Muehling, Raasch & Gebhardt, P.A.  
STREET: 119 No. US20020068814A1th Fourth Street  
CITY: Minneapolis

STATE: MN  
COUNTRY: USA  
ZIP: 55401

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,345  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: McCormack, Myra H  
REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 180.00020101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/305-1228  
TELEFAX: 612/305-1228

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:

LENGTH: 52 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-09-813-345-14

Query Match 28.5%; Score 72.5; DB 9; Length 52;  
Best Local Similarity 38.5%; Pred. No. 0.067;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTCOVONLSHRLMQLMGPAGQDSAPVDPSSPHSY 47  
DB 15 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRKSISPQGY 52

RESULT 3  
US-10-197-954-2  
Sequence 2, Application US/10197954  
Publication No. US20030119021A1

GENERAL INFORMATION:  
APPLICANT: Kuster, Hubert  
APPLICANT: Siddiqui, Suhail

APPLICANT: Little, Daniel  
TITLE OF INVENTION: Capture Compounds, Collections Thereof  
TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex  
TITLE OF INVENTION: Compositions  
FILE REFERENCE: 24743-2305

CURRENT APPLICATION NUMBER: US/10/197,954  
CURRENT FILING DATE: 2002-07-16

PRIOR APPLICATION NUMBER: 60/306,019  
PRIOR FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: 60/314,123  
PRIOR FILING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: 60/363,433  
PRIOR FILING DATE: 2002-03-11

NUMBER OF SEQ ID NOS: 149  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2  
LENGTH: 52  
TYPE: PRT

ORGANISM: Homo Sapien  
US-10-197-954-2

Query Match 28.5%; Score 72.5; DB 14; Length 52;  
Best Local Similarity 38.5%; Pred. No. 0.067;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTCOVONLSHRLMQLMGPAGQDSAPVDPSSPHSY 47  
DB 15 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRKSISPQGY 52

## RESULT 4

US-10-474-635A-19  
Sequence 19, Application US/10474635A  
Publication No. US20040176567A1

GENERAL INFORMATION:  
APPLICANT: Isis Innovation Ltd

TITLE OF INVENTION: Peptides  
FILE REFERENCE: 480821.00004

CURRENT APPLICATION NUMBER: US/10/474,635A  
CURRENT FILING DATE: 2003-10-14

PRIOR APPLICATION NUMBER: GB 0109438.2  
PRIOR FILING DATE: 2001-04-17

NUMBER OF SEQ ID NOS: 22  
SOFTWARE: Patent in version 3.1

SEQ ID NO 19  
LENGTH: 52  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-474-635A-19

Query Match 28.5%; Score 72.5; DB 16; Length 52;  
Best Local Similarity 38.5%; Pred. No. 0.067;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTCOVONLSHRLMQLMGPAGQDSAPVDPSSPHSY 47  
DB 15 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRKSISPQGY 52

RESULT 5  
US-10-718-071-43  
Sequence 43, Application US/10718071  
Publication No. US20050009847A1

GENERAL INFORMATION:  
APPLICANT: Bertilsson, Goran  
APPLICANT: Eriandsson, Rikard

APPLICANT: Friesen, Jonas  
APPLICANT: Haegerstrand, Anders

APPLICANT: Heidrich, Jessica  
APPLICANT: Hellstrom, Kristina

APPLICANT: Haggblad, Johan  
APPLICANT: Jansson, Katarina

APPLICANT: Korlesmaa, Jarkko  
US-10-718-071-43

```

; APPLICANT: Lindquist, Per
; APPLICANT: Lundh, Hanna
; APPLICANT: McGuire, Jacqueline
; APPLICANT: Mercer, Alex
; APPLICANT: Nyberg, Karl
; APPLICANT: Ossolnak, Amna
; APPLICANT: Patrone, Cesare
; APPLICANT: Ronnholm, Harriet
; APPLICANT: Wikstrom, Lilian
; APPLICANT: Zachrisson, Olof
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS
; FILE REFERENCE: 21882-517 UTIL
; CURRENT APPLICATION NUMBER: US/10/718,071
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US 60/427,912
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-718-071-43

```

```

Query Match 28.5%; Score 72.5; DB 17; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.067;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```

```

OY 9 GCVLGTCOVONLSHRLMQLMGPAKODSAPVDSPSHSY 47
Db 15 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRSKISPGY 52

RESULT 6
US-10-760-085-2
; Sequence 2, Application US/10760085
; Publication No. US20050042771A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K"ster
; APPLICANT: Daniel Paul Little
; APPLICANT: Sunaib Mahmood Siddiqi
; APPLICANT: Matthew Peter Greallish
; APPLICANT: Subramaniam Mareppan
; APPLICANT: Chester Frederick Haseman III
; APPLICANT: Ping Yip
; TITLE OF INVENTION: Capture Compounds, Collections Thereof
; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex
; FILE REFERENCE: 24743-2309
; CURRENT APPLICATION NUMBER: US/10/760,085
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: 60/441,398
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo Saplen
US-10-760-085-2

```

```

Query Match 28.5%; Score 72.5; DB 17; Length 52;
Best Local Similarity 38.5%; Pred. No. 0.067;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```

```

OY 9 GCVLGTCOVONLSHRLMQLMGPAKODSAPVDSPSHSY 47
Db 15 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRSKISPGY 52

RESULT 7
US-10-364-889-6
; Sequence 6, Application US/10364889

```

```

; Publication No. US20030224989A1
; GENERAL INFORMATION:
; APPLICANT: Pabel, Gregory L.
; APPLICANT: Quinn, Kerry
; TITLE OF INVENTION: Compositions and Methods for Treatment of Osteoarthritis
; FILE REFERENCE: 21402-558
; CURRENT APPLICATION NUMBER: US/10/364,889
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/356,376
; PRIOR FILING DATE: 2002-02-12
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 6
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-889-6

```

```

Query Match 28.5%; Score 72.5; DB 15; Length 185;
Best Local Similarity 38.5%; Pred. No. 0.27;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```

```

OY 9 GCVLGTCOVONLSHRLMQLMGPAKODSAPVDSPSHSY 47
Db 109 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRSKISPGY 146

RESULT 8
US-10-372-683-12
; Sequence 12, Application US/10372683
; Publication No. US20040009171A1
; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PERLS JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 12
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo saplen
US-10-372-683-12

```

```

Query Match 28.5%; Score 72.5; DB 15; Length 185;
Best Local Similarity 38.5%; Pred. No. 0.27;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

```

```

OY 9 GCVLGTCOVONLSHRLMQLMGPAKODSAPVDSPSHSY 47
Db 109 GCRFGTCVQKLAHQIYQFT-DKDKNVAPRSKISPGY 146

RESULT 9
US-10-675-406A-7
; Sequence 7, Application US/10675406A
; Publication No. US20040121375A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Pharmaceuticals Corporation
; APPLICANT: Eweleigh, Deepra
; APPLICANT: Taylor, Ian
; TITLE OF INVENTION: METHODS FOR PREDICTION AND PROGNOSIS OF CANCER, AND MONITORING
; FILE REFERENCE: 5138
; CURRENT APPLICATION NUMBER: US/10/675,406A
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: US 60/415,194

```

PRIOR FILING DATE: 2002-09-30  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 7  
LENGTH: 185  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-675-406A-7

Query Match  
Best Local Similarity 38.5%; Score 72.5; DB 16; Length 185;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQOVNLSHRLMQLMGPAQRODSAPVDPSSPHSY 47  
Db 109 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRKSISFGY 146

RESULT 10  
US-10-755-889-148  
Sequence 148, Application US/10755889  
Publication No. US20040171823A1  
GENERAL INFORMATION:  
APPLICANT: Bristol-Myers Squibb Company  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB  
FILE REFERENCE: D0284 NP  
CURRENT APPLICATION NUMBER: US/10/755,889  
CURRENT FILING DATE: 2004-01-13  
PRIOR APPLICATION NUMBER: U.S. 60/440,068  
PRIOR FILING DATE: 2003-01-14  
PRIOR APPLICATION NUMBER: U.S. 60/469,757  
PRIOR FILING DATE: 2003-05-12  
NUMBER OF SEQ ID NOS: 823  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 148  
LENGTH: 185  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-755-889-148

\* Query Match  
Best Local Similarity 38.5%; Score 72.5; DB 16; Length 185;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQOVNLSHRLMQLMGPAQRODSAPVDPSSPHSY 47  
Db 109 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRKSISFGY 146

RESULT 11  
US-09-813-345-15  
Sequence 15, Application US/09813345  
Patent No. US20020068814A1  
GENERAL INFORMATION:  
APPLICANT: Smith, Derek D.  
Sana, Shankar  
Abel, Peter W.  
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR  
SUPERFAMILY AND METHODS OF USE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Meeting, Raasch & Gebhardt, P.A.  
STREET: 119 No. US20020068814A1ch Fourth Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/813,345  
FILING DATE: 20-Mar-2001  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: McCormack, Myra H  
REGISTRATION NUMBER: 36,602  
REFERENCE/DOCKET NUMBER: 180.00020101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/305-1220  
TELEFAX: 612/305-1228  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 50 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
US-09-813-345-15

Query Match  
Best Local Similarity 27.4%; Score 69.5; DB 9; Length 50;  
Matches 14; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQOVNLSHRLMQLMGPAQRODSAPVDPSSPHSY 47  
Db 13 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRKSISFGY 50

RESULT 12  
US-10-718-071-16  
Sequence 16, Application US/10718071  
Publication No. US2005009847A1  
GENERAL INFORMATION:  
APPLICANT: Bertilsson, Goran  
APPLICANT: Erlandsson, Rikard  
APPLICANT: Friesen, Jonas  
APPLICANT: Haegerstrand, Anders  
APPLICANT: Heidrich, Jessica  
APPLICANT: Hellstrom, Kristina  
APPLICANT: Hagblad, Johan  
APPLICANT: Jansson, Katarina  
APPLICANT: Kortessmaa, Jarkko  
APPLICANT: Lindquist, Per  
APPLICANT: Lundh, Hanna  
APPLICANT: McGuire, Jacqueline  
APPLICANT: Mercer, Alex  
APPLICANT: Nyberg, Karl  
APPLICANT: Ossolinak, Amina  
APPLICANT: Patrone, Cesare  
APPLICANT: Ronnholm, Harriet  
APPLICANT: Wikstrom, Lilian  
APPLICANT: Zachrisson, Olof  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR INCREASING NEUROGENESIS  
FILE REFERENCE: 21882-517 UTIL  
CURRENT APPLICATION NUMBER: US/10/718,071  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: US 60/427,912  
PRIOR FILING DATE: 2002-11-20  
NUMBER OF SEQ ID NOS: 71  
SOFTWARE: Patentin version 3.2  
SEQ ID NO 16  
LENGTH: 52  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-718-071-16

Query Match  
Best Local Similarity 38.5%; Score 68.5; DB 17; Length 52;  
Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 9 GCVLGTQOVNLSHRLMQLMGPAQRODSAPVDPSSPHSY 47

Db 15 GCRFGTCTVQKLAHQIYQFT-DKDKONVAPRSKISPGY 52

## RESULT 13

US-10-264-237-1622  
; Sequence 1622, Application US/10264237  
; Publication No. US20040009491A1  
; GENERAL INFORMATION:  
; APPLICANT: Birse et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PA131P1  
; CURRENT APPLICATION NUMBER: US/10/264,237  
; CURRENT FILING DATE: 2002-10-04  
; PRIOR APPLICATION NUMBER: PCT/US01/16450  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/205,515  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 2876  
; SOFTWARE: PatentIn Ver. 3.1  
; SEQ ID NO 1622  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (62)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (67)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (71)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (102)  
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids  
US-10-264-237-1622

Query Match 25.2%; Score 64; DB 15; Length 103;  
Best Local Similarity 40.0%; Pred. No. 1.8;  
Matches 18; Conservative 5; Mismatches 14; Indels 8; Gaps 3;

QY 2 QAOQLRVGCVLGTCCQVONLSHRLWQMGPAGRDSDAPVDPSSPHS 46  
Db 8 QAOQLDSDGC-QQTSPLDPDNNHAW-ILGPPS-----LDPRSPTS 44

## RESULT 14

US-10-437-963-198108  
; Sequence 198108, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barabak, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 198108  
; LENGTH: 216  
; TYPE: PRT

; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_93800C.1.pcp  
US-10-437-963-198108

Query Match 25.0%; Score 63.5; DB 16; Length 216;  
Best Local Similarity 31.0%; Pred. No. 4.7;  
Matches 13; Conservative 13; Mismatches 11; Indels 5; Gaps 1;

QY 6 LRVGCVLGTCCQVONLSHRLWQMGPAGRDSDAPVDPSSPHS 42  
Db 19 LGRGIIITGCEVTSVSNRGLFAVNRVHGSGSRKQTAEIDPS 60

## RESULT 15

US-10-360-101-74  
; Sequence 74, Application US/10360101  
; Publication No. US20040009550A1  
; GENERAL INFORMATION:  
; APPLICANT: Moll, Gert N.  
; APPLICANT: Leenhouts, Cornelis J.  
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way  
; FILE REFERENCE: 2183-5673  
; CURRENT APPLICATION NUMBER: US/10/360,101  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR APPLICATION NUMBER: EP 02077060.8  
; PRIOR FILING DATE: 2002-05-24  
; NUMBER OF SEQ ID NOS: 309  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 74  
; LENGTH: 52  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: A13,S16-sequence of Adrenomedullin Hypotensive peptide  
US-10-360-101-74

Query Match 24.6%; Score 62.5; DB 15; Length 52;  
Best Local Similarity 35.9%; Pred. No. 1.4;  
Matches 14; Conservative 6; Mismatches 18; Indels 1; Gaps 1;

QY 9 GCVLGTCCQVONLSHRLWQMGPAGRDSDAPVDPSSPHS 47  
Db 15 GSRFGTCTVQKLAHQIYQFT-DKDKONVAPRSKISPGY 52

Search completed: May 4, 2005, 18:27:15  
Job time: 135 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 17:56:39 ; Search time 162 Seconds  
(without alignments)  
112.208 Million cell updates/sec

Title: US-10-723-368-5  
Perfect score: 254  
Sequence: 1 TQQLRVGCVLTGCVQNL.....MGPAQRDSAPVDPSSPHSY 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	254	100.0	47	AD061523	AD061523 Human int
2	254	100.0	148	AD061520	AD061520 Human int
3	76	29.9	52	AA091765	AA091765 Adrenomed
4	72.5	28.5	52	AA091759	AA091759 Adrenomed
5	72.5	28.5	52	AA075110	AA075110 Human adr
6	72.5	28.5	52	AA09818	AA09818 Human adr
7	72.5	28.5	52	ABP55104	ABP55104 Human adr
8	72.5	28.5	52	ADCC2152	ADCC2152 Human adr
9	72.5	28.5	52	ADG91993	ADG91993 Human mat
10	72.5	28.5	52	ADM94034	ADM94034 Human AM
11	72.5	28.5	52	ADN03278	ADN03278 Exemplantary
12	72.5	28.5	52	ADM98309	ADM98309 Mature hu
13	72.5	28.5	52	ADP18429	ADP18429 Neurogene
14	72.5	28.5	52	ADP18402	ADP18402 Neurogene
15	72.5	28.5	52	ADP42113	ADP42113 Adrenomed
16	72.5	28.5	53	AA075111	AA075111 Glycine e
17	72.5	28.5	53	AA075112	AA075112 Glycine e
18	72.5	28.5	53	ABJ18665	ABJ18665 Universal
19	72.5	28.5	62	AA075113	AA075113 linker pe
20	72.5	28.5	91	ADP55556	ADP55556 Active hu
21	72.5	28.5	120	AA075123	AA075123 Usppa(1-56
22	72.5	28.5	120	AA075122	AA075122 Usppa(1-57
23	72.5	28.5	120	ABJ18669	ABJ18669 Universal
24	72.5	28.5	120	ABJ18670	ABJ18670 Universal
25	72.5	28.5	147	AA075124	AA075124 Usppa(1-84

26	72.5	28.5	147	ABJ18671	ABJ18671 Universal
27	72.5	28.5	170	AA075114	AA075114 Thioedox
28	72.5	28.5	185	AA060344	AA060344 Human adr
29	72.5	28.5	185	AA049697	AA049697 Human adr
30	72.5	28.5	185	ABP72347	ABP72347 Adrenomed
31	72.5	28.5	185	AD027595	AD027595 Human adr
32	72.5	28.5	185	ADP55557	ADP55557 Human adr
33	72.5	28.5	185	ADN10849	ADN10849 Human adr
34	72.5	28.5	185	ADM98308	ADM98308 Human pre
35	72.5	28.5	185	ADP18855	ADP18855 Human pre
36	72.5	28.5	185	ADP12587	ADP12587 Protein e
37	72.5	28.5	185	AD036937	AD036937 Human pro
38	72.5	28.5	185	AD014147	AD014147 Human NF
39	72.5	28.5	185	ADR87608	ADR87608 Human adr
40	72.5	28.5	185	ADP19162	ADP19162 Human adr
41	72.5	28.5	186	ADP18582	ADP18582 Human dis
42	72.5	28.5	206	ABJ18668	ABJ18668 Universal
43	71.5	28.1	184	ABJ57209	ABJ57209 Mouse 18c
44	71.5	28.1	184	AD060040	AD060040 CRH signa
45	70.5	27.8	188	AA060345	AA060345 Porcine a

## ALIGNMENTS

RESULT 1  
AD061523  
ID AD061523 standard; protein; 47 AA.  
XX  
AC AD061523;  
XX  
DT 26-AUG-2004 (first entry)  
XX  
DE Human intermedin mature proetin SEQ ID NO:5.  
XX  
KW human; intermedin; hypotensive; gene therapy; hypertension;  
KW cardioprotective; diet; prolactin release; growth hormone release;  
KW ovarian follicle survival; oedema.  
XX  
OS Homo sapiens.  
XX  
FN MO2004048547-A2.  
XX  
PD 10-JUN-2004.  
XX  
PF 26-NOV-2003; 2003MO-US037968.  
XX  
PR 26-NOV-2002; 2002US-0429327P.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PI Heu SYT;  
XX  
DR WPI; 2004-441176/41.  
XX  
PT New composition comprises an intermedin peptide, useful for treating  
PT hypertension, as cardioprotective agent, as a diet aid, for the release  
PT of prolactin, or for growth hormone release from the pituitary.  
XX  
PS Disclosure; SEQ ID NO 5; 68pp; English.  
XX  
CC The invention relates to a novel composition comprising an intermedin  
CC peptide, which comprises at least 18 contiguous amino acids in a sequence  
CC comprising 148 amino acids (AD061520). A composition of the invention has  
CC hypotensive activity, and may have a use in gene therapy. The composition  
CC comprising the intermedin peptide is useful for identifying homologous or  
CC related genes, for production of the encoded peptide, in producing  
CC compositions that modulate the expression or function of its encoded  
CC protein, for gene therapy, mapping functional regions of the protein, or  
CC in studying associated physiological pathways. The intermedin peptide is  
CC useful for treating hypertension, as a cardioprotective agent, as a diet  
CC aid, for the release of prolactin, in growth hormone release from the  
CC pituitary, or for ovarian follicle survival and growth. They are also

CC useful in the reduction of oedema. The present sequence represents the  
CC human intermedin mature protein.

XX  
SQ Sequence 47 AA;

Query Match 100.0%; Score 254; DB 8; Length 47;  
Best Local Similarity 100.0%; Pred. No. 1.1e-27;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQAQLRVGCVLTGTCVQVNTLSHRLWQLMGPAGRODSAPVDPSSPHSY 47  
DB 1 TQAQLRVGCVLTGTCVQVNTLSHRLWQLMGPAGRODSAPVDPSSPHSY 47

## RESULT 2

AD061520  
ID AD061520 standard; protein; 148 AA.

AC- AD061520;

XX 26-AUG-2004 (first entry)

DE Human intermedin SEQ ID NO:2.

XX human; intermedin; hypotensive; gene therapy; hypertension;

KW cardioprotective; diet; prolactin release; growth hormone release;

KW ovarian follicle survival; oedema.

XX Homo sapiens.

PN WO2004048547-A2.

XX 10-JUN-2004.

XX 26-NOV-2003; 2003WO-US037968.

XX 26-NOV-2002; 2002US-0429327P.

XX (STRD ) UNIV LELAND STANFORD JUNIOR.

PI Hsu SYT;

DR WPI; 2004-441176/41.

DR N-PSDB; AD061519.

XX New composition comprises an intermedin peptide, useful for treating  
PT hypertension, as cardioprotective agent, as a diet aid, for the release  
PT of prolactin, or for growth hormone release from the pituitary.

XX Claim 1; SEQ ID NO 2; 68pp; English.

XX The invention relates to a novel composition comprising an intermedin  
CC peptide, which comprises at least 18 contiguous amino acids in a sequence  
CC comprising 148 amino acids (AD061520). A composition of the invention has  
CC hypotensive activity, and may have a use in gene therapy. The composition  
CC comprising the intermedin peptide is useful for identifying homologous or  
CC related genes, for production of the encoded peptide, in producing  
CC compositions that modulate the expression or function of its encoded  
CC protein, for gene therapy, mapping functional regions of the protein, or  
CC in studying associated physiological pathways. The intermedin peptide is  
CC useful for treating hypertension, as a cardioprotective agent, as a diet  
CC aid, for the release of prolactin, in growth hormone release from the  
CC pituitary, or for ovarian follicle survival and growth. They are also  
CC useful in the reduction of oedema. The present sequence represents the  
CC human intermedin protein of the invention.

XX Sequence 148 AA;

Query Match 100.0%; Score 254; DB 8; Length 148;  
Best Local Similarity 100.0%; Pred. No. 3.9e-27;  
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TQAQLRVGCVLTGTCVQVNTLSHRLWQLMGPAGRODSAPVDPSSPHSY 47

DB 101 TQAQLRVGCVLTGTCVQVNTLSHRLWQLMGPAGRODSAPVDPSSPHSY 147

RESULT 3  
AAB91765  
ID AAB91765 standard; peptide; 52 AA.

XX AAB91765;

XX 22-JUN-2001 (first entry)

DE Adrenomedullin peptide (AM) SEQ ID NO:941.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimide; maleimide group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

PN WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US013576.

XX 17-MAY-1999; 99US-0134406P.

XX 10-SEP-1999; 99US-0153406P.

XX 15-OCT-1999; 99US-0159783P.

XX (CONG-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity.

XX Disclosure; Page 501; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimide and maleimide groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity in  
CC vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB9441 represent peptides which can be used in the  
CC exemplification of the present invention

XX Sequence 52 AA;

Query Match 29.9%; Score 76; DB 4; Length 52;  
Best Local Similarity 35.9%; Pred. No. 0.0091;  
Matches 14; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 9 GCVLGTGVQVNTLSHRLWQLMGPAGRODSAPVDPSSPHSY 47  
DB 14 GCRGTGVQVNTLSHRLWQLMGPAGRODSAPVDPSSPHSY 52

RESULT 4  
AAB91759



ID AAB91759 standard; peptide; 52 AA.  
 XX  
 AC AAB91759;  
 XX  
 XX 22-JUN-2001 (first entry)  
 XX  
 DE Adrenomedullin peptide (AM) SEQ ID NO:935.  
 XX  
 KM Protection; endogenous therapeutic peptide; peptidase; conjugation;  
 KM blood component; modification; succinimide; maleimido group; amino;  
 KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX  
 PN WO200069900-A2.  
 XX  
 PD 23-NOV-2000.  
 XX  
 PF 17-MAY-2000; 2000WO-US013576.  
 XX  
 PR 17-MAY-1999; 99US-0134406P.  
 PR 10-SEP-1999; 99US-0153406P.  
 PR 15-OCT-1999; 99US-0159783P.  
 XX  
 PA (CONJ-) CONJUCHEM INC.  
 XX  
 PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
 XX  
 .DR WPI; 2001-112059/12.  
 XX  
 PT Modifying and attaching therapeutic peptides to albumin prevents  
 PT peptidase degradation, useful for increasing length of in vivo activity.  
 XX  
 PS Disclosure; Page 498; 733pp; English.  
 XX  
 CC The present invention describes a modified therapeutic peptide (I)  
 CC comprising a therapeutically active amino acid region (III) and a  
 CC reactive group (II) (e.g. succinimide) and maleimido groups attached to  
 CC a less therapeutically active amino acid region (IV), which covalently  
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.  
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
 CC factors and neurotransmitters, to protect them from peptidase activity in  
 CC vivo for the treatment of various disorders. Endogenous therapeutic  
 CC peptides are not suitable as drug candidates as they require frequent  
 CC administration due to rapid degradation by peptidases in the body.  
 CC Modifying and attaching therapeutic peptides to albumin prevents or  
 CC reduces the action of peptidases to increase length of activity (half  
 CC life) and specifically as bonding to large molecules decreases  
 CC intracellular uptake and interference with physiological processes.  
 CC AAB90829 to AAB92441 represent peptides which can be used in the  
 CC exemplification of the present invention  
 XX  
 SO Sequence 52 AA;  
 XX  
 Query Match 28.5%; Score 72.5; DB 4; Length 52;  
 Best Local Similarity 38.5%; Pred. No. 0.028;  
 Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;  
 XX  
 OY 9 GCVLGTGVONLISHRLWQLMGAPGDSAPVDSPSPSY 47  
 DB 15 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRSKISPOGY 52  
 XX  
 RESULT 5  
 ID AAB75110 standard; protein; 52 AA.  
 XX  
 AC AAB75110;  
 XX  
 DT 31-JUL-2001 (first entry)  
 XX

DE Human adrenomedullin (AM) protein.  
 XX  
 KM Adrenomedullin; glycine extended adrenomedullin; AM; AM-gly;  
 KM adrenomedullin precursor; fusion protein; pharmaceutical; diagnostic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200127310-A1.  
 XX  
 PD 19-APR-2001.  
 XX  
 PF 10-OCT-2000; 2000WO-JP007023.  
 XX  
 PR 15-OCT-1999; 99JP-00294147.  
 XX  
 PA (SHIO) SHIONOGI & CO LTD.  
 XX  
 PI Takimoto A, Mitsuda Y, Nakayama T, Mitsuhashi K;  
 XX  
 .DR WPI; 2001-282044/29.  
 DR N-PSDB; AAH19806.  
 XX  
 PT Producing adrenomedullin useful for pharmaceutical and diagnostic  
 PT application comprises producing fused adrenomedullin precursor using a  
 PT recombinant host.  
 XX  
 PS Disclosure; Page 45; 75pp; Japanese.  
 XX  
 CC The present invention describes a method (M1) for producing  
 CC adrenomedullin precursor. The method comprises: (a) producing the fused  
 CC protein using a recombinant host cell; (b) restricted digestion of the  
 CC fused protein by a protease followed by collection of sediment; and (c)  
 CC dissolving the sediment and extracting adrenomedullin precursor. The  
 CC method can be used for the production of adrenomedullin precursor for  
 CC pharmaceutical and diagnostic applications. AAH19806 to AAH19866 and  
 CC AAB75110 to AAB75124 represent sequences which are used in the  
 CC exemplification of the present invention  
 XX  
 SO Sequence 52 AA;  
 XX  
 Query Match 28.5%; Score 72.5; DB 4; Length 52;  
 Best Local Similarity 38.5%; Pred. No. 0.028;  
 Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;  
 XX  
 OY 9 GCVLGTGVONLISHRLWQLMGAPGDSAPVDSPSPSY 47  
 DB 15 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRSKISPOGY 52  
 XX  
 RESULT 6  
 ID AAE09818 standard; peptide; 52 AA.  
 XX  
 AC AAE09818;  
 XX  
 DT 29-NOV-2001 (first entry)  
 XX  
 DE Human adrenomedullin peptide #1.  
 XX  
 KM Human; vasoactive peptide; calcitonin gene related peptide; CGRP;  
 KM CGRP-receptor identification; adrenomedullin.  
 XX  
 OS Homo sapiens.  
 OS  
 XX  
 PN US6268474-B1.  
 PN  
 PD 31-JUL-2001.  
 XX  
 PF 30-APR-1998; 98US-00070504.  
 XX  
 PR 30-APR-1998; 98US-00070504.  
 XX  
 PA (UYCR-) UNIV CREIGHTON.  
 XX



RESULT 9  
ADG91993  
ID ADG91993 standard; protein; 52 AA.  
XX  
AC ADG91993;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Human mature adrenomedullin protein.  
XX  
KW neuroleptic; antisense therapy; gene therapy; adrenomedullin agonist;  
KW schizophrenia; gene expression; decidua protein induced by progesterone;  
KW DPP; adrenomedullin; cold shock domain protein A; csa; antisense;  
KW siRNA; ribozyme; triple helix formation.  
XX  
OS Homo sapiens.  
XX  
PN WO2003078658-A2.  
XX  
PD 25-SEP-2003.  
XX  
PF 19-MAR-2003; 2003WO-EP002875.  
XX  
PR 20-MAR-2002; 2002US-0366001P.  
XX  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS PHARMA GMBH.  
XX  
PI Buxton FP, Carpenter WT, Roberts RC, Tamminga CA;  
XX  
DR WPI; 2003-767532/72.  
XX  
PT Screening for schizophrenia in a population utilizing genes encoding the  
PT decidua protein induced by progesterone, adrenomedullin and/or cold  
PT shock domain protein A, useful in diagnosing, preventing and/or treating  
PT schizophrenia.  
XX  
XX  
PS Disclosure; SEQ ID NO 1; 41pp; English.  
XX  
CC The invention relates to a method of screening for schizophrenia in a  
CC population comprising determining the magnitude of expression, in members  
CC of the population, of at least one gene selected from the gene encoding  
CC decidua protein induced by progesterone (DPP), the gene encoding  
CC adrenomedullin and the gene encoding cold shock domain protein A (csa)  
CC in a sample, and comparing the magnitude of expression to a baseline of  
CC expression of the gene, where increased gene expression indicates the  
CC presence of schizophrenia. An antisense molecule, siRNA, ribozyme or  
CC nucleic acid molecule promoting triple helix formation that specifically  
CC inhibit the expression of DPP, csa or adrenomedullin genes, is useful  
CC for the manufacture of a medicament for the treatment of schizophrenia.  
CC An antibody that specifically binds an epitope of DPP, csa or  
CC adrenomedullin is also useful for the manufacture of a medicament for the  
CC treatment of schizophrenia. This sequence represents the mature  
CC adrenomedullin protein.  
XX  
SQ Sequence 52 AA;  
XX  
Query Match 28.5%; Score 72.5; DB 7; Length 52;  
Best Local Similarity 38.5%; Pred. No. 0.028;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;  
OY 9 GCVTGTCOVNLSHRLQWLMGPAGRODAPVDPSPSY 47  
DB 15 GCRFGTCTVOKLHAQIYQFT-DKDXNVAPRSKISPOGY 52

DT 17-JUN-2004 (first entry)  
XX  
XX Human AM peptide, a CRSP homologue.  
DE  
XX  
KW calcitonin receptor stimulating peptide; CRSP; cAMP activity;  
KW skeletal disorder; cancer; hypertension; restenosis; analgesic;  
KW appetite suppressant; diuretic; vasotrophic; cytoskeletal; diuretic;  
KW osteopathic; anorectic; hypotensive; human; AM.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
FH Disulfide-bond 16..21  
FT Modified-site 52  
FT /note="C-terminal amide"  
XX  
XX WO2003102180-A1.  
XX  
XX  
XX 11-DEC-2003.  
XX  
XX 28-MAY-2003; 2003WO-JP006641.  
XX  
XX 04-JUN-2002; 2002JP-00162797.  
XX  
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
XX (NINA-) JAPAN NAT CARDIOVASCULAR.  
XX  
XX Minamino N, Katafuchi T;  
XX  
XX WPI; 2004-043113/04.  
XX  
XX  
XX Calcitonin receptor stimulating peptide promoting cAMP production in  
PT cells for treatment of cancer; skeletal disorders and hypertension and as  
PT appetite suppressants and analgesics.  
XX  
XX  
PS Disclosure; Fig 2; 62pp; Japanese.  
XX  
CC This invention relates to novel calcitonin receptor stimulating peptides  
CC (CRSPs) that are expressed in the central nervous system and act on the  
CC calcitonin receptor to promote the production of cAMP within a cell.  
CC Specifically, it refers to CRSPs that can stimulate concentration  
CC dependent sodium ion uptake and furthermore act to inhibit calcium ion  
CC uptake by the cell. The present invention describes mutant peptides  
CC derived from the CRSPs that have additions, deletions and/or  
CC substitutions of one or more amino acids, yet that retain similar  
CC activity and are useful for developing drug compositions and  
CC pharmaceutically acceptable carriers to treat and/or prevent skeletal  
CC disorders, cancer, hypertension and restenosis. Furthermore, CRSPs can  
CC also be used as analgesics, appetite suppressants and diuretics such that  
CC exhibit vasotropic, cytoskeletal, diuretic, osteopathic, anorectic and  
CC hypotensive activities. This peptide sequence is a human AM peptide that  
CC has cAMP activity, given in an exemplification of the invention.  
XX  
SQ Sequence 52 AA;  
XX  
Query Match 28.5%; Score 72.5; DB 8; Length 52;  
Best Local Similarity 38.5%; Pred. No. 0.028;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;  
OY 9 GCVTGTCOVNLSHRLQWLMGPAGRODAPVDPSPSY 47  
DB 15 GCRFGTCTVOKLHAQIYQFT-DKDXNVAPRSKISPOGY 52

RESULT 11  
ADN03278  
ID ADN03278 standard; peptide; 52 AA.  
XX  
AC ADN03278;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
XX Exemplary peptide ligand for proteome analysis #2.



KM neural tissue G-protein coupled receptor activator; neurogenesis inducer;  
 KM intracellular neural Ca 2+ enhancer; intracellular neural cAMP stimulator;  
 KM intracellular neural Ca 2+ enhancer; Parkinson's disease;  
 KM Parkinson's disorder; Huntington's disease; Alzheimer's disease;  
 KM multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;  
 KM progressive supranuclear palsy; Lewy body disease; spinal ischemia;  
 KM ischemic stroke; cerebral infarction; spinal cord injury;  
 KM cancer-related brain; spinal cord injury; multi-infarct dementia;  
 KM geriatric dementia; cAMP level; embryonic tissue; human.  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO2004045592-A2.  
 XX  
 PD 03-JUN-2004.  
 XX  
 XX 20-NOV-2003; 2003MO-IB005311.  
 XX  
 XX 20-NOV-2002; 2002US-0427912P.  
 XX  
 XX (NEUR-) NEURONOVA AB.  
 PA (BERT) BERTILSSON G.  
 PA (ERLA) ERLANDSSON R.  
 PA (FRIS) FRISSEN J.  
 PA (HAEG) HAEGSTRAND A.  
 PA (HEID) HEIDRICH J.  
 PA (HEIL) HEILSTROM K.  
 PA (HAEG) HAEGBLAD J.  
 PA (JANS) JANSSON K.  
 PA (KORT) KORTESMAA J.  
 PA (LUND) LINDQUIST P.  
 PA (LUND) LUNDH H.  
 PA (MCGU) MCGUIRE J.  
 PA (MERC) MERCER A.  
 PA (NJB) NJBERG K.  
 PA (OSSO) OSSOINAK A.  
 PA (PATR) PATRONE C.  
 PA (ROEN) ROENHOLM H.  
 PA (ZACH) ZACHRISSON O.  
 PA (WIKS) WIKSTROM L.  
 XX  
 XX Bertilsson G, Eriandsson R, Frissen J, Haegstrand A, Heidrich J;  
 PI Hellstroem K, Haegblad J, Jansson K, Kortesmaa J, Lindquist P;  
 PI Lundh H, Meguire J, Mercer A, Njberg K, Ossoinak A, Patrone C;  
 PI Roenholm H, Zachrisson O, Wikstrom L;  
 DR WPI; 2004-449666/42.  
 XX  
 XX Use of agent(s) that elevate intracellular cyclic adenosine monophosphate  
 PT or intracellular calcium levels in neural tissue for modulating  
 PT neurogenesis to treat central nervous system disorder.  
 XX  
 XX Disclosure; SEQ ID NO 43; 77pp; English.  
 XX  
 XX This invention relates to a novel method of modulating neurogenesis in  
 CC the neural tissue of a patient exhibiting symptom(s) of a central nervous  
 CC system disorder, such as neurodegenerative, ischemic or learning and  
 CC memory disorder or neurological trauma. The method involves at least one  
 CC agent (A) that elevates intracellular cyclic adenosine monophosphate  
 CC (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+  
 CC levels in the neural tissue, which is administered where (A) modulates  
 CC and (B) induces neurogenesis. The invention may be useful for the  
 CC production of compounds with a neurotropic, neuroprotective, CNS-Gen,  
 CC cerebroprotective, vasotropic, anticonvulsant, antiparkinsonian,  
 CC haemostatic, hypertensive, muscular-Gen, ophthalmological,  
 CC antiinflammatory, analgesic or antidiabetic activity. These compounds may  
 CC act as neurogenesis modulators, neural stem or progenitor cell  
 CC proliferation, differentiation and/or migration modulators, neural tissue  
 CC G-protein coupled receptor activators, neurogenesis inducers,  
 CC intracellular neural cAMP enhancers, intracellular neural cAMP  
 CC stimulators or intracellular neural Ca 2+ enhancers. The invention is  
 CC useful for modulating neurogenesis in neural tissue of a patient  
 CC exhibiting at least one symptom of central nervous system disorder, such

CC as Parkinson's disease and Parkinson's disorders, Huntington's disease,  
 CC Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis,  
 CC Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease,  
 CC spinal ischemia, ischemic stroke, cerebral infarction, spinal cord  
 CC injury, cancer-related brain and spinal cord injury, multi-infarct  
 CC dementia, and geriatric dementia; for increasing the intracellular levels  
 CC of or stimulating cAMP levels in a cell (preferably a cell from a neural  
 CC tissue); and for in vitro modulation of neurogenesis. The agent modulates  
 CC neurogenesis in neural tissue by modulating proliferation,  
 CC differentiation, migration or survival of neural stem cells or progenitor  
 CC cells in the tissue; by maintaining or increasing the amount or  
 CC percentage of doublecortin positive cells in the neural tissue relative  
 CC to a patient not dosed with the agent or by activation of a G-protein  
 CC coupled receptor in the neural tissue. The method results in elevation of  
 CC cAMP levels of the neural stem cells by over 20% compared to untreated  
 CC tissue. The in vivo induction of neurogenesis allows treatment of  
 CC disorders caused by cell loss, injury or disease by endogenous  
 CC replacement and obviates the need for transplanting foreign cells into a  
 CC patient. Neurogenesis can also be induced by administration of the  
 CC neurogenesis-modulating agent directly into a desired site, which avoids  
 CC unnecessary systemic administration and possible side effects and further  
 CC provides an alternative to the use of drugs and the controversial use of  
 CC large quantities of embryonic tissue for treatment of Parkinson's  
 CC disease. The present sequence is that of a polypeptide which has been  
 CC shown to have the ability to increase intracellular cAMP levels and which  
 CC is related to the method of the invention.  
 XX  
 XX Sequence 52 AA;  
 SQ  
 Query Match 28.5%; Score 72.5; DB 8; Length 52;  
 Best Local Similarity 38.5%; Pred. No. 0.028;  
 Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;  
 QY 9 GCVLTGQVONLSHRMLMGPRGDSAPVDSSPSHY 47  
 Db 15 GCRFGTCVOKLAHQIVQFT-DXDKQNVAPRSKISPOGY 52  
 RESULT 14  
 ADP18402  
 ID ADP18402 standard; protein; 52 AA.  
 AC ADP18402;  
 DT 26-AUG-2004 (first entry)  
 XX  
 XX Neurogenesis modulation-related protein Segidp16.  
 DE  
 XX neurogenesis modulation; neural tissue; central nervous system disorder;  
 KM neurodegenerative; ischemic; learning and memory disorder;  
 KM neurological trauma; neurotropic; neuroprotective; CNS-Gen;  
 KM cerebroprotective; vasotropic; anticonvulsant; antiparkinsonian;  
 KM haemostatic; hypertensive; muscular-Gen; ophthalmological;  
 KM antiinflammatory; analgesic; antidiabetic; neurogenesis modulator;  
 KM neural stem cell; progenitor cell;  
 KM neural tissue G-protein coupled receptor activator; neurogenesis inducer;  
 KM intracellular neural cAMP enhancer; intracellular neural cAMP stimulator;  
 KM intracellular neural Ca 2+ enhancer; Parkinson's disease;  
 KM Parkinson's disorder; Huntington's disease; Alzheimer's disease;  
 KM multiple sclerosis; amyotrophic lateral sclerosis; Shy-Drager syndrome;  
 KM progressive supranuclear palsy; Lewy body disease; spinal ischemia;  
 KM ischemic stroke; cerebral infarction; spinal cord injury;  
 KM cancer-related brain; spinal cord injury; multi-infarct dementia;  
 KM geriatric dementia; cAMP level; embryonic tissue; human.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO2004045592-A2.  
 XX  
 XX 03-JUN-2004.  
 PD  
 XX 20-NOV-2003; 2003MO-IB005311.  
 XX

20-NOV-2002; 2002US-0427912P.

XX (NEUR-) NEURONOVA AB.  
 PA (BERT) BERTILSSON G.  
 PA (ERLA) ERLANDSSON R.  
 PA (FRIS) FRISSEN J.  
 PA (HAEG) HAEGSTRAND A.  
 PA (HEID) HEIDRICH J.  
 PA (HELL) HELSTROEM K.  
 PA (HAEG) HAEGBLAD J.  
 PA (JANS) JANSSON K.  
 PA (KORT) KORTESMAA J.  
 PA (LIND) LINDQUIST P.  
 PA (LUND) LUNDH H.  
 PA (MCGU) MCGUIRE J.  
 PA (MERC) MERCER A.  
 PA (NUBE) NUBERG K.  
 PA (OSSO) OSSOINAK A.  
 PA (PATR) PATRONE C.  
 PA (ROEN) ROENNHOLOM H.  
 PA (ZACH) ZACHRISSON O.  
 PA (WIKS) WIKSTROEM L.

XX Bertilsson G, Erlandsson R, Frisen J, Haegstrand A, Heidrich J;  
 PI Hellstroem K, Haegblad J, Jansson K, Kortesmaa J, Lindquist P;  
 PI Lundh H, McGuire J, Mercer A, Njberg K, Ossoinak A, Patrone C;  
 PI Roenholm H, Zachrisson O, Wikstroem L;

DR WPI; 2004-449666/42.

PT Use of agent (s) that elevate intracellular cyclic adenosine monophosphate  
 or intracellular calcium levels in neural tissue for modulating  
 neurogenesis to treat central nervous system disorder.

PS Disclosure; SEQ ID NO 16; 77bp; English.

XX This invention relates to a novel method of modulating neurogenesis in  
 CC the neural tissue of a patient exhibiting symptom(s) of a central nervous  
 CC system disorder, such as neurodegenerative, ischemic or learning and  
 CC memory disorder or neurological trauma. The method involves at least one  
 CC agent (A) that elevates intracellular cyclic adenosine monophosphate  
 CC (cAMP) levels or at least one agent (B) that elevates intracellular Ca 2+  
 CC levels in the neural tissue, which is administered where (A) modulates  
 CC and (B) induces neurogenesis. The invention may be useful for the  
 CC production of compounds with a neurotropic, neuroprotective, CNS-Gen,  
 CC neuroprotective, vasotropic, anticonvulsant, antiparkinsonian,  
 CC haemostatic, hypertensive, muscular-gen, ophthalmological,  
 CC antiinflammatory, analgesic or antidiabetic activity. These compounds may  
 CC act as neurogenesis modulators, neural stem or progenitor cell  
 CC proliferation, differentiation and/or migration modulators, neural tissue  
 CC G-protein coupled receptor activators, neurogenesis inducers,  
 CC intracellular neural cAMP enhancers, intracellular neural cAMP  
 CC stimulators or intracellular neural Ca 2+ enhancers. The invention is  
 CC useful for modulating neurogenesis in neural tissue of a patient  
 CC exhibiting at least one symptom of central nervous system disorder, such  
 CC as Parkinson's disease and Parkinson's disorders, Huntington's disease,  
 CC Alzheimer's disease, multiple sclerosis, amyotrophic lateral sclerosis,  
 CC Shy-Drager syndrome, progressive supranuclear palsy, Lewy body disease,  
 CC spinal ischaemia, ischaemic stroke, cerebral infarction, spinal cord  
 CC injury, cancer-related brain and spinal cord injury, multi-infarct  
 CC dementia and geriatric dementia; for increasing the intracellular levels  
 CC of or stimulating cAMP levels in a cell (preferably a cell from a neural  
 CC tissue); and for in vitro modulation of neurogenesis. The agent modulates  
 CC neurogenesis in neural tissue by modulating proliferation,  
 CC differentiation, migration or survival of neural stem cells or progenitor  
 CC cells in the tissue; by maintaining or increasing the amount or  
 CC percentage of doublecortin positive cells in the neural tissue relative  
 CC to a patient not dosed with the agent or by activation of a G-protein  
 CC coupled receptor in the neural tissue. The method results in elevation of  
 CC cAMP levels of the neural stem cells by over 20% compared to untreated  
 CC tissue. The in vivo induction of neurogenesis allows treatment of  
 CC disorders caused by cell loss, injury or disease by endogenous  
 CC replacement and obviates the need for transplanting foreign cells into a

CC patient. Neurogenesis can also be induced by administration of the  
 CC neurogenesis-modulating agent directly into a desired site, which avoids  
 CC unnecessary systemic administration and possible side effects and further  
 CC provides an alternative to the use of drugs and the controversial use of  
 CC large quantities of embryonic tissue for treatment of Parkinson's  
 CC disease. The present sequence is that of a polypeptide which has been  
 CC shown to have the ability to increase intracellular cAMP levels and which  
 CC is related to the method of the invention.

XX Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;

Best Local Similarity 38.5%; Pred. No. 0.028; Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCYLGTQYQVNTSHRLMQLMPAGRODSAPVDPSPHSY 47  
 DB 15 GCRFGTCTVQKLAHQIYQFT-DKDXDNVAPRSKISFOGY 52

RESULT 15

ID ADR42113 standard; peptide; 52 AA.

XX ADR42113;

XX 21-OCT-2004 (first entry)

DE Adrenomedullin related peptide ligand, SEQ ID 2.

KW Human; ligand; Adrenomedullin.

XX Homo sapiens.

PN WO2004064972-A2.

PD 05-AUG-2004.

XX 16-JAN-2004; 2004WO-US001037.

PR 16-JAN-2003; 2003US-0441398P.

XX (HKPH-) HK PHARM INC.

PA (KOSK-) KOESTER H.

PI Koester H, Little DP, Siddiqi SM, Grealish MP, Marappan S;

PI Haseman CF, Yip P;

DR WPI; 2004-642213/62.

PT Identifying drug non-target biomolecules in mixture of biomolecules  
 PT involves interacting mixture of biomolecules with capture compounds  
 PT having high binding affinity and analyzing captured biomolecules to  
 PT identify drug non-targets.

PS Disclosure; SEQ ID NO 2; 368bp; English.

XX The present invention relates to a method for identifying drug non-target  
 CC biomolecules in a mixture of biomolecules. The method comprises  
 CC interacting mixture with capture compounds having moiety X which  
 CC covalently binds to biomolecules with high affinity, moiety Y that  
 CC increases selectivity of binding so that the capture compound binds to  
 CC fewer biomolecules, and moiety Z for presenting X and Y, and analyzing  
 CC captured biomolecules to identify drug non-targets. The capture compound  
 CC also optionally comprises a sorting function moiety Q and or a solubility  
 CC function moiety W. The selectivity function moiety Y serves to modulate  
 CC the reactivity function by reducing the number of groups to which the  
 CC reactivity function moiety X binds, such as by steric hindrance and other  
 CC interactions. Y is optionally a peptide ligand (ADR42112-ADR42256).

XX Sequence 52 AA;

Query Match 28.5%; Score 72.5; DB 8; Length 52;

Best Local Similarity 38.5%; Pred. No. 0.028;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCCTGTCQVONTLSRLMQLMGPAQRDSAPVDPSSPHSY 47  
Db 15 GCRFGCTVOKLAHQIYQFT-DKDDNVAVPRSKISPOGY 52

Search completed: May 4, 2005, 18:11:09  
Job time : 164 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 17:57:34 ; Search time 176 Seconds  
(without alignments)  
136.748 Million cell updates/sec

Title: US-10-723-368-5

Sequence: 1 TQQLRVGCVLGTQVQNL.....MGPRGRDAPVDPSSPHSY 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	254	100.0	148	1	ADM2_HUMAN
2	228	89.8	150	1	Q7Z4H4 homo sapien
3	225	88.6	146	1	ADM2_RAT
4	188	74.0	159	2	Q75XW6
5	187	73.6	168	2	Q75XW7
6	185.5	73.0	140	2	Q61F59
7	87.5	34.4	174	2	Q75XW8
8	83	32.7	123	2	Q75XW4
9	78.5	30.9	171	2	Q61R85
10	72.5	28.5	185	1	ADM2_HUMAN
11	71.5	28.1	184	1	ADM2_MOUSE
12	71.5	28.1	188	1	ADM2_BOVIN
13	71.5	28.1	188	2	Q95K00
14	70.5	27.8	188	2	ADM2_PIG
15	70	27.6	927	2	Q75S75
16	69.5	27.4	185	1	ADM2_RAT
17	69.5	27.4	188	1	ADM2_CANFA
18	64	25.2	388	2	Q68Y70
19	63	24.8	798	2	Q68Y70
20	59	23.2	142	2	Q6P390
21	59	23.2	386	2	Q7Z4H4
22	59	23.2	506	2	Q6D6B0
23	58.5	23.0	576	2	Q6N2F7
24	58.5	23.0	1281	2	Q6N2F7
25	58	22.8	281	2	Q93RX1
26	58	22.8	339	2	Q8YGC6
27	58	22.8	351	2	Q6TRC2
28	58	22.8	516	2	Q9P775
29	58	22.8	557	2	Q6G1J5
30	58	22.8	557	2	Q6G1J5
31	58	22.8	559	2	Q9GW71

32	58	22.8	1306	2	Q95QM6	Q95QM6 caenorhabdi
33	58	22.8	1544	2	Q19194	Q19194 caenorhabdi
34	58	22.8	1557	2	Q8WPK9	Q8WPK9 oikopleura
35	57	22.4	82	2	Q6ERN3	Q6ERN3 oryza sativ
36	57	22.4	810	1	ZCC5_HUMAN	Q9C0U0 homo sapien
37	57	22.4	810	1	ZCC5_MOUSE	Q9C148 mus musculu
38	57	22.4	810	2	Q6E822	Q6E822 canis fami
39	57	22.4	811	2	Q7ZWS6	Q7ZWS6 xenopus lae
40	57	22.4	1057	2	Q701Z9	Q701Z9 anopheles g
41	57	22.4	1784	2	Q94606	Q94606 leishmania
42	56.5	22.2	521	2	Q61NA0	Q61NA0 homo sapien
43	56	22.0	184	2	Q92N11	Q92N11 rhizobium m
44	55.5	21.9	411	2	Q99PY2	Q99PY2 streptomyces
45	55.5	21.9	528	2	Q88R34	Q88R34 pseudomonas

## ALIGNMENTS

RESULT 1	ADM2_HUMAN	STANDARD;	PRT;	148 AA.
ID	Q7Z4H4			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Adrenomedullin 2 precursor (intermedin) [containing: Adrenomedullin 2 (intermedin-long) (IMDL); intermedin-short (IMDS)].			
GN	Name=ADM2; Synonyms=AM2;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.			
RX	PubMed=1615490; DOI=10.1074/jbc.M305332200;			
RA	Roh J., Chang C.L., Bhalla A., Klein C., Hsu S.Y.T.;			
RT	"Intermedin is a calcitonin/calcitonin gene-related peptide family			
RT	peptide acting through the calcitonin receptor-like receptor/receptor			
RT	activity-modifying protein receptor complex."			
RL	J. Biol. Chem. 279:7264-7274(2004).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney;			
RX	PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;			
RA	Takel Y., Houe K., Ogoshi M., Kawahara T., Sannai H., Miyano S.;			
RT	"Identification of novel adrenomedullin in mammals: a potent			
RT	cardiovascular and renal regulator."			
RL	FEBS Lett. 556:53-58(2004).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;			
RA	Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,			
RA	Clump M., Smink L.J., Alnecough R., Almeida J.P., Babbage A.K.,			
RA	Bagnoley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,			
RA	Bird C.P., Blakey S.E., Brideman A.M., Buck D., Burgess J., Clark G.,			
RA	Burill W.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,			
RA	Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,			
RA	Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,			
RA	Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,			
RA	Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,			
RA	Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,			
RA	Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,			
RA	Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King A.,			
RA	Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M.,			
RA	Martin I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T.,			
RA	McClay C.N., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,			
RA	Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,			
RA	Scott C.B., Sena H.K., Skuce C.D., Smalley S., Smith W.L.,			
RA	Soderlund C., Spragon L., Steward C.A., Sultson J.E., Swann R.M.,			
RA	Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,			
RA	Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,			

RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
 RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kodoh J.,  
 RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,  
 RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,  
 RA Dorman A., Fang F., Fu Y., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malai E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren O., Shalli S., Sloan D., Song L.,  
 RA Wang O., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,  
 RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mink P.,  
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,  
 RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,  
 RA Korfi I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,  
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saita S.,  
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,  
 RA O'Brien K.P., Wilkison P., Bodenteich A., Tapia I., Bruder C.E.,  
 RA Khan A.S., Lane L., Tiliakou Y., Wright H., Hartman K., Hu X.,  
 RA "The DNA sequence of human chromosome 22.";  
 RT Nature 402:489-495(1999).  
 CC -1- FUNCTION: IMDL and IMDS may play a role as physiological  
 CC regulators of gastrointestinal, cardiovascular bioactivities  
 CC mediated by the CALCRL/RAMPs receptor complexes. Activates the  
 CC CAMP-dependent pathway.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed in the esophagus, stomach, jejunum,  
 CC ileum, ileocecum, ascending colon, transverse colon, descending  
 CC colon and rectum.  
 CC -1- SIMILARITY: Belongs to the adrenomedullin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF529213; AAC09100.1; -;  
 CC EMBL: AB121034; BAD07411.1; -;  
 CC EMBL: AL096767; -; NOT ANNOTATED\_CDS.  
 CC Genew: HGNC:28898; ADM2.  
 CC MIM: 608682; -;  
 CC KMW Amdation: Cleavage on pair of basic residues; Hormone; Signal.  
 CC FT SIGNAL: 1 24  
 CC FT PROPEP: 25 98  
 CC FT PEPTIDE: 101 147 By similarity.  
 CC FT PEPTIDE: 108 147 Adrenomedullin 2 (By similarity).  
 CC FT DISULFID: 110 115 Intermedin-short (Potential).  
 CC FT MOD\_RES: 147 147 Tyrosine amide (G-148 provides amide  
 CC group) (Probable).  
 CC SQ SEQUENCE 148 AA; 15865 MW; 680E3098CCE5BF2 CRC64;  
 CC  
 CC Query Match 100.0%; Score 254; DB 1; Length 148;  
 CC Best Local Similarity 100.0%; Pred. No. 1.2e-24;  
 CC Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 CC  
 CC QY 1 TQAQLRVCVIGTCOVONLSHRLWQMGPRGRDSAPVDPSSPSHY 47  
 CC DB 101 TQAQLRVCVIGTCOVONLSHRLWQMGPRGRDSAPVDPSSPSHY 147  
 CC  
 CC RESULT 2  
 CC ADM2\_MOUSE  
 CC ID ADM2\_MOUSE STANDARD; PRT; 150 AA.  
 CC AC Q7TNK8;  
 CC DT 05-JUL-2004 (Rel. 44, Created)  
 CC DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 CC DE Adrenomedullin 2 precursor (Intermedin) (Contains: Adrenomedullin 2  
 CC (Intermedin-long) (IMDL); Intermedin-short (IMDS)).

GN Name=Adm2; Synonyms=Am2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 RN NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC STRAIN=C57BL/6;  
 RX PubMed=14615490; DOI=10.1074/jbc.M305332200;  
 RA Roh J., Chang C.L., Bhalla A., Klein C., Heu S.Y.T.,  
 RA "Intermedin is a calcitonin/calcitonin gene-related peptide family  
 RA peptide acting through the calcitonin receptor-like receptor/receptor  
 RA activity-modifying protein receptor complexes.";  
 RA J. Biol. Chem. 279:7264-7274(2004).  
 RN [2]  
 RP SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.  
 RC TISSUE=Kidney;  
 RX PubMed=14706825; DOI=10.1016/S0014-5793(03)01368-1;  
 RA Takei Y., Inoue K., Ogoshi M., Kawahara T., Bannai H., Miyano S.,  
 RA "Identification of novel adrenomedullin in mammals: a potent  
 RA cardiovascular and renal regulator.";  
 RA FEBS Lett. 536:53-58(2004).  
 CC -1- FUNCTION: IMDL and IMDS may play a role as physiological  
 CC regulators of gastrointestinal, cardiovascular bioactivities  
 CC mediated by the CALCRL/RAMPs receptor complexes. Activates the  
 CC CAMP-dependent pathway.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: High expression detected in the submaxillary  
 CC gland, kidney, stomach, and mesentery, followed by the pituitary,  
 CC lung, pancreas, intestines, spleen, thymus and ovary. Expressed  
 CC mainly in the intermediate lobe of the pituitary, with sporadic in  
 CC the anterior lobe.  
 CC -1- SIMILARITY: Belongs to the adrenomedullin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF529213; AAC09099.1; -;  
 CC EMBL: AB121035; BAD07412.1; -;  
 CC MGD: MGI:2675256; Adm2.  
 CC DR MGD: MGI:2675256; Adm2.  
 CC KMW Amdation: Cleavage on pair of basic residues; Hormone; Signal.  
 CC FT SIGNAL: 1 25  
 CC FT PROPEP: 26 100  
 CC FT PEPTIDE: 103 149 By similarity.  
 CC FT PEPTIDE: 110 149 Adrenomedullin 2 (By similarity).  
 CC FT DISULFID: 112 117 Intermedin-short (Potential).  
 CC FT MOD\_RES: 149 149 Tyrosine amide (G-150 provides amide  
 CC group) (Probable).  
 CC SQ SEQUENCE 150 AA; 16188 MW; 2BF392BFBFDBBA CRC64;  
 CC  
 CC Query Match 89.8%; Score 228; DB 1; Length 150;  
 CC Best Local Similarity 93.3%; Pred. No. 2.6e-21;  
 CC Matches 42; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 CC  
 CC QY 3 AQLIRVCVIGTCOVONLSHRLWQMGPRGRDSAPVDPSSPSHY 47  
 CC DB 105 AQLIRVCVIGTCOVONLSHRLWQMGPRGRDSAPVDPSSPSHY 149  
 CC  
 CC RESULT 3  
 CC ADM2\_RAT  
 CC ID ADM2\_RAT STANDARD; PRT; 146 AA.  
 CC AC P61312;  
 CC DT 05-JUL-2004 (Rel. 44, Created)  
 CC DT 05-JUL-2004 (Rel. 44, Last sequence update)  
 CC DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 CC DE Adrenomedullin 2 precursor (Intermedin) (Contains: Adrenomedullin 2  
 CC (Intermedin-long) (IMDL); Intermedin-short (IMDS)).

[illegible]

RT CRLR/RAMP receptor complexes.",  
 RL J. Biol. Chem. 0:0-0(2003).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Heu S.Y.T.;  
 RL Submitted (NOV-2003) to the EMBL/genbank/DBJ databases.  
 CC -1- MISCELLANEOUS: The sequence shown here is derived from an  
 CC EMBL/genbank/DBJ third party annotation (TPA) entry.  
 DR EMBL; BK004089; DAA0455.1; --  
 FT NON\_TER  
 SQ SEQUENCE 140 AA; 15816 MW; 509F74908C0DC75D CRC64;  
 Query Match 73.0%; Score 185.5; DB 2; Length 140;  
 Best Local Similarity 77.3%; Pred. No. 7,2e-16;  
 Matches 34; Conservative 7; Mismatches 2; Indels 1; Gaps 1;

RESULT 7	
075XW8	
ID	PRELIMINARY; PRT; 174 AA.
AC	075XW8;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Adrenomedullin-1.
GN	Name=ADM1;
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC	Tetraodontidae; Tetraodontidae; Takifugu.
OX	NCBI_TaxID=31033;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22984567; PubMed=14623291; DOI=10.1016/j.dbrc.2003.10.111;
RA	Ogoshi M., Inoue K., Takel Y.;
RT	"Identification of a novel adrenomedullin gene family in teleost fish."
RL	Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR	EMBL; AB120285; BAD02341.1; -
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005179; F:hormone activity; IEA.
SQ	SEQUENCE 174 AA; 20222 MW; 61535B41FCF88D4D CRC64;
Query Match	
Best Local Similarity	34.4%; Score 87.5; DB 2; Length 174;
Matches 21; Conservative	53.8%; Pred. No. 0.0038;
	3; Mismatches 14; Indels 1; Gaps 1;
Qy	9 GCVLGTCOVQVLSHRLWQLMPCAGROSPAPVPSPSHSY 47
Db	95 GCSLGCTVADLAFRLHQL-GFYKIDIAVPDKISPSQY 132
RESULT 8	
ID	075XW4
AC	075XW4;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Adrenomedullin-5.
GN	Name=ADM5;
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC	Tetraodontidae; Tetraodontidae; Takifugu.
OX	NCBI_TaxID=31033;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22984567; PubMed=14623291; DOI=10.1016/j.dbrc.2003.10.111;
RA	Ogoshi M., Inoue K., Takel Y.;
RT	"Identification of a novel adrenomedullin gene family in teleost fish."
RL	Biochem. Biophys. Res. Commun. 311:1072-1077(2003).
DR	EMBL; AB120285; BAD02341.1; -
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0005179; F:hormone activity; IEA.
SQ	SEQUENCE 174 AA; 20222 MW; 61535B41FCF88D4D CRC64;

[illegible]

RESULT 9			
06L8KS			
ID	06L8KS	PRELIMINARY;	PRT; 171 AA.
AC	06L8KS;		
DT	05-JUL-2004 (TREMBLrel. 27, Created)		
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)		
DE	Preproadrenomedullin precursor.		
GN	Name=preproAM;		
OS	Cyprius carpio (Common carp).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;		
OC	Cyprinidae; Cyprinus.		
CC	NCBI_TaxID=7962;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Liver;		
RX	PubMed=15242754; DOI=10.1016/j.yjgen.2004.05.002;		
RA	Kondo T., Sakai M.;		
RT	"Molecular cloning and expression of preproadrenomedullin gene from		
RL	Gen. Comp. Endocrinol. 136:78-88(2004).		
DR	EMBL; AB120940; BAD19046.1; -		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0005179; F:hormone activity; IEA.		
DR	InterPro; IPR001710; Adrenomedullin.		
DR	PRINTS; PR00801; ADRENOMEDULLIN.		
KW	SIGNAL.		
FT	SIGNAL	1	23 Potential.
FT	CHAIN	79	127 adrenomedullin.
SQ	SEQUENCE	171 AA;	19412 MW; A9595B9A11E5AC36 CRC64;
Query Match 30.9%; Score 78.5; DB 2; Length 171;			
Best Local Similarity 42.2%; Pred. No. 0.053;			
Matches 19; Conservative 5; Mismatches 20; Indels 1; Gaps 1;			
QY	3 AQLLRVGCVLGTCOVQNIISHRLQMLMGAPAGRODPAPVDPSPSHSY 47		
DB	84 SQRSRSCSGTCTVHYLAHRLHDLNKKL-KIGNAPADKLNPFQY 127		
RESULT 10			
ADML_HUMAN			
ID	ADML_HUMAN	STANDARD;	PRT; 185 AA.
AC	P35318;		
DT	01-FEB-1994 (Rel. 28, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	ADM Precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20		
DE	terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].		
GN	Name=ADM; Synonyms=AM;		
OS	Homo sapiens (human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
CC	NCBI_TaxID=9606;		

[1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Pheochromocytoma;  
 RX MEDLINE=93343928; PubMed=7688224;  
 RA Kitamura K., Sakata J., Kangawa K., Kojima M., Matsuo H., Eto T.,  
 RT "Cloning and characterization of cDNA encoding a precursor for human  
 RL adrenomedullin.";  
 RL Biochem. Biophys. Res. Commun. 194:720-725(1993).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94354869; PubMed=8074714;  
 RA Ishihara T., Kojima M., Kangawa K., Hino J., Matsuo H.,  
 RA Kitamura K., Eto T., Matsuo H.,  
 RT "Genomic structure of human adrenomedullin gene.";  
 RL Biochem. Biophys. Res. Commun. 203:631-639(1994).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausberg R.L., Peinhold E.A., Grouse L.H., Derge J.G.,  
 RA Klausberg R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uddin T.B., Toehlyuk S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Bosak S.A., McWeney K.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kelleman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalek U., Smallus D.E.,  
 RA Scherf A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [4]  
 RP SEQUENCE OF 95-146.  
 RC TISSUE=Pheochromocytoma;  
 RX MEDLINE=93249425; PubMed=8387282;  
 RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Nakamura S.,  
 RA Matsuo H., Eto T.,  
 RT "Adrenomedullin: a novel hypotensive peptide isolated from human  
 RL pheochromocytoma.";  
 RL Biochem. Biophys. Res. Commun. 192:553-560(1993).  
 [5]  
 RP REVIEW.  
 RX MEDLINE=98240137; PubMed=9578982; DOI=10.1006/brne.1998.0164;  
 RA Samson W.K.,  
 RT "Proadrenomedullin-derived peptides.";  
 RL Front. Neuroendocrinol. 19:100-127(1998).  
 [6]  
 RP REVIEW.  
 RX MEDLINE=20053666; PubMed=10588445; DOI=10.1016/S0167-0115(99)00025-7;  
 RA Champion H.C., Nussdorfer G.G., Kadowitz P.J.,  
 RT "Structure-activity relationships of adrenomedullin in the circulation  
 RL and adrenal gland.";  
 RL Regul. Pept. 85:1-8(1999).  
 -1- FUNCTION: AM and PAMP are potent hypotensive and vasodilator  
 agents. Numerous actions have been reported most related to the  
 physiologic control of fluid and electrolyte homeostasis. In the  
 kidney, am is diuretic and natriuretic, and both am and pamp  
 inhibit aldosterone secretion by direct adrenal actions. In  
 pituitary gland, both peptides at physiologically relevant doses  
 inhibit basal ACTH secretion. Both peptides appear to act in brain  
 and pituitary gland to facilitate the loss of plasma volume,  
 actions which complement their hypotensive effects in blood  
 vessels.  
 -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Highest levels found in pheochromocytoma and  
 CC adrenal medulla. Also found in lung, ventricle and kidney tissues.  
 CC -1- SIMILARITY: Belongs to the adrenomedullin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; D14874; BAA03589.1; -  
 DR EMBL; S73906; AAC60642.1; -  
 DR EMBL; BC015861; AAH15961.1; -  
 DR EMBL; D43639; BAA07756.1; ALT\_SEQ.  
 DR PIR; JC2351; JN0684.  
 DR Genem; HGNC:259; ADM.  
 DR H-InvDB; HIK0009441; -  
 DR MIM; 103275; -  
 DR GO; GO:0005615; Cytoplasmic space; TAS.  
 DR GO; GO:0005625; Cytoplasmic fraction; TAS.  
 DR GO; GO:0005102; Receptor binding; TAS.  
 DR GO; GO:0006171; P-camp biosynthesis; TAS.  
 DR GO; GO:0007267; P-cell-cell signaling; TAS.  
 DR GO; GO:0008015; P-circulation; TAS.  
 DR GO; GO:0007565; P-pregnancy; TAS.  
 DR GO; GO:0006701; P-progesterone biosynthesis; TAS.  
 DR GO; GO:0009611; P-response to wounding; TAS.  
 DR GO; GO:0007165; P-signal transduction; TAS.  
 DR InterPro; IPR001710; Adrenomedullin.  
 DR Pfam; PF02039; Adrenomedullin; 1.  
 DR PRINTS; PRO0801; ADRENOMEDULLIN.  
 KW Amdaction; Cleavage on pair of basic residues;  
 KW Direct protein sequencing; Hormone; Polymorphism; Signal.  
 FT SIGNAL 22 21  
 FT PEPTIDE 1 21  
 FT PROPEP 45 92  
 FT PROPEP 148 185  
 FT DISULFID 110 115  
 FT MOD\_RES 41 41  
 FT MOD\_RES 146 146  
 FT MOD\_RES 146 146  
 FT VARIANT 50 50  
 FT FT  
 SQ SEQUENCE 185 AA; 20420 MW; 64C7D2A0B4654DFB CRC64;  
 Query Match 28.5%; Score 72.5; DB 1; Length 185;  
 Best Local Similarity 38.5%; Pred. No. 0.34; Indels 1; Gaps 1;  
 Matches 15; Conservative 6; Mismatches 17;  
 Db 109 GCVLGTGVONLSHRLQMLGAPVDSPPSHSY 47  
 9 GCVLGTGVONLSHRLQMLGAPVDSPPSHSY 47  
 109 GCVLGTGVONLSHRLQMLGAPVDSPPSHSY 47  
 RESULT 11  
 ADML\_MOUSE STANDARD; PRT; 184 AA.  
 AC P97257; P97453;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20  
 DE terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].  
 GN Name-Adm.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

[illegible]

```

OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Aorta;
RX MEDLINE=98244567; PubMed=9585168; DOI=10.1016/S0024-3205(98)00079-4;
RA Barker S., Wood E., Clark A.J.L., Corder R.;
RT "Cloning of bovine preproadrenomedullin and inhibition of its basal
RL expression in vascular endothelial cells by staurosporine."
CC Life Sci. 62:11407-1415(1998).
CC -I- FUNCTION: Hypotensive peptide. May function as a hormone in
CC circulation control (By similarity).
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- SIMILARITY: Belongs to the adrenomedullin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ001613; CAA04866.1; -.
DR InterPro; IPR001710; Adrenomedullin.
DR Pfam; PF02039; Adrenomedullin.1.
DR PRINTS; PR00801; ADRENOMEDULLIN.
KW Amidation; Cleavage on pair of basic residues; Hormone; Signal.
FT SIGNAL 1 21 By similarity.
FT PEPTIDE 22 41 Proadrenomedullin N-20 terminal peptide.
FT PROPEP 45 92 By similarity.
FT PEPTIDE 95 146 Adrenomedullin.
FT PROPEP 148 188 PreproAM C-terminal fragment (By
FT similarity).
FT DISULFID 110 115 By similarity.
FT MOD_RES 41 41 Arginine amide (G-42 provides amide
FT group) (By similarity).
FT MOD_RES 146 146 Tyrosine amide (G-147 provides amide
FT group) (By similarity).
SQ SEQUENCE 188 AA; 20981 MW; 3002E79AB3B6612C CRC64;

Query Match 28.1%; Score 71.5; DB 1; Length 188;
Best Local Similarity 38.5%; Pred. No. 0.47;
Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 9 GCVLGTGVQVONTSHRLWQLMGPAQRDQSAFVDSSPSHSY 47
Db 109 GCRFGTCVTVOGLAHQIVHFT-DKDKDSAPRSKRSPGKY 146
||| ||| |::| |||
||| ||| |::| |||

RESULT 13
O95SKPO PRELIMINARY; PRT; 188 AA.
Q95SKPO AC O95KPO;
DT 01-DEC-2001 (TREMBLrel.19, Created)
DT 01-DEC-2001 (TREMBLrel.19, Last sequence update)
DE 01-MAR-2004 (TREMBLrel.26, Last annotation update)
DE Adrenomedullin.
GN Name=DBAM-2;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Butheraia; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
[1]
RN NAME=SEQUENCE FROM N.A.
RP MEDLINE=21630318; PubMed=11754956; DOI=10.1016/S0196-9781(01)00529-0;
RA Kitamura K., Matsui E., Kato J., Katoh F., Kita T., Tsuji T.,
RT "Adrenomedullin (11-26): a novel endogenous hypotensive peptide
RL isolated from bovine adrenal medulla."
RR Peptides 22:1713-1718(2001).
RR EMBL; AB055107; BAB62176.1; -.

```

DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR001710; Adrenomedullin.  
 DR Pfam; PF02039; Adrenomedullin; 1.  
 DR PRINTS; PR00801; ADRENOMEDULLIN.  
 SQ SEQUENCE 188 AA; 20963 MW; 6102869A756DCAB6 CRC64;  
 Query Match 28.1%; Score 71.5; DB 2; Length 188;  
 Best Local Similarity 38.5%; Pred. No. 0.47;  
 Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;  
 QY 9 GCVLGTCQVONLSHRLWQLMGPAGRODSAPVDPSSPSHY 47  
 Db 109 GCRFGTCVTQKLAHQIYHFT-DKDKGASAPRSKISPGY 146  
 RESULT 14  
 ID ADML\_PIG STANDARD; PRT; 188 AA.  
 AC P53366;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE ADM precursor [Contains: Adrenomedullin (AM); Proadrenomedullin N-20 terminal peptide (ProAM-N20) (ProAM N-terminal 20 peptide) (PAMP)].  
 GN Name=ADM; Synonyms=AM;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Adrenal medulla;  
 RA MEDLINB=94139945; PubMed=8043068; DOI=10.1016/0014-5793(94)80289-0;  
 RA Kitamura K., Kangawa K., Kojima M., Ichiki Y., Matsuo H., Eto T.;  
 RT "Complete amino acid sequence of porcine adrenomedullin and cloning of  
 RT cDNA encoding its precursor."  
 RL FEBS Lett. 338:306-310(1994).  
 RN [2]  
 RP SEQUENCE OF 22-41.  
 RC TISSUE=Adrenal medulla;  
 RA MEDLINB=94357274; PubMed=8076689; DOI=10.1016/0014-5793(94)00810-8;  
 RA Kitamura K., Kangawa K., Ishiyama Y., Washimine H., Ichiki Y.,  
 RA Kawamoto M., Minamino N., Matsuo H., Eto T.;  
 RT "Identification and hypotensive activity of proadrenomedullin N-  
 RT terminal 20 peptide (PAMP)."  
 RL FEBS Lett. 351:35-37(1994).  
 CC -1- FUNCTION: AM and PAMP are potent hypotensive and vasodilator  
 CC agents.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Highly expressed in adrenal glands, lung and  
 CC kidney.  
 CC -1- SIMILARITY: Belongs to the adrenomedullin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; D14875; BA03590.1; -.  
 DR PIR; S41600; S41600.  
 DR InterPro; IPR001710; Adrenomedullin.  
 DR InterPro; IPR01038; Calycin.  
 DR Pfam; PF02039; Adrenomedullin; 1.  
 DR PRINTS; PR00801; ADRENOMEDULLIN.  
 KM Amidation; Cleavage on pair of basic residues;  
 KM Direct protein sequencing; Hormone; Signal.  
 FT SIGNAL 1 21  
 FT PEPTIDE 22 92 Proadrenomedullin N-20 terminal peptide.  
 FT PROPEP 45 92

FT PEPTIDE 95 146 Adrenomedullin.  
 FT PROPEP 153 188 PreproAM C-terminal fragment (By  
 FT similarity).  
 FT DISULFID 110 115 By similarity.  
 FT MOD\_RES 41 41 Arginine amide (G-42 provides amide  
 FT group).  
 FT MOD\_RES 146 146 Tyrosine amide (G-147 provides amide  
 FT group).  
 SQ SEQUENCE 188 AA; 20893 MW; 71749460F5660A61 CRC64;  
 Query Match 27.8%; Score 70.5; DB 1; Length 188;  
 Best Local Similarity 38.5%; Pred. No. 0.63;  
 Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;  
 QY 9 GCVLGTCQVONLSHRLWQLMGPAGRODSAPVDPSSPSHY 47  
 Db 109 GCRFGTCVTQKLAHQIYHFT-DKDKGASAPRSKISPGY 146  
 RESULT 15  
 ID Q7S575 PRELIMINARY; PRT; 927 AA.  
 AC Q7S575;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Hypothetical protein.  
 GN Name=NCU02295.1;  
 OS Neurospora crassa.  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
 OX NCBI\_TaxID=5141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=OR74A;  
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,  
 RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
 RA Qui D., Ianakiev P., Pedersen D., Nelson E.L., Washburne M.,  
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,  
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,  
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gheire S.,  
 RA Kamal M., Kamyshev S.M., Mauceli E., Bielke C., Rudd S., Prihman D.,  
 RA Kryzofowa S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,  
 RA Cogoni C., Macino G., Cacheseide D., Li W., Pratt R.J., Omani S.A.,  
 RA D'Souza C.C., Glaes L., Orbach M.J., Berglund J., Voelker K.,  
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,  
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,  
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;  
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."  
 RL Nature 010-0(2003).  
 CC -1- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBD whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -----  
 DR EMBL; AABX01000355; EAA30703.1; -.  
 DR HSSP; P78356; 1B01.  
 DR GO; GO:0016308; F:1-phosphatidylinositol-4-phosphate 5-kinase. . .; IEA.  
 DR InterPro; IPR002498; PI5K.  
 DR Pfam; PF01504; PI5K; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 927 AA; 102558 MW; 21FDCA9FA419E932 CRC64;  
 Query Match 27.6%; Score 70; DB 2; Length 927;  
 Best Local Similarity 72.2%; Pred. No. 4.2;  
 Matches 13; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 30 PACGRDAPVDPSSPSHY 47  
 Db 123 PACGRDAPVDPSSPSHY 140

Search completed: May 4, 2005, 18:14:12  
 Job time : 178 secs





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 17:58:05 ; Search time 39 Seconds  
(Without alignments)  
115.954 Million cell updates/sec

Title: US-10-723-368-5

Sequence: 1 TQQLRVACVLTGTCQVNL.....MGPGRQDSAPVPSPHSY 47

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79: \*  
2: pirt: \*  
3: pirt3: \*  
4: pirt4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.5	28.5	185	2 JN0684	adrenomedullin pre
2	70.5	27.8	188	2 S41600	adrenomedullin - p
3	69.5	27.4	185	2 JN0766	adrenomedullin pre
4	58	22.8	339	2 AC3406	1-lactate permease
5	58	22.8	560	2 A38731	alpha-1A adenosyl
6	58	22.8	1544	2 T29482	hypothetical prote
7	57	22.4	1784	2 T02844	cdcl1-related prot
8	54	21.3	283	2 E82662	ABC transporter AT
9	54	21.3	792	2 T26050	hypothetical prote
10	53.5	21.1	303	2 A43708	gamma-interferon-1
11	53.5	21.1	345	2 A37845	carboxylesterase (
12	53	20.9	136	2 T35335	hypothetical prote
13	53	20.9	192	2 AE2414	hypothetical prote
14	53	20.9	272	2 H95954	probable Sir2-like
15	53	20.9	351	2 E97187	cytochrome P450 4A6
16	53	20.9	450	2 S07051	cysteine proteinase
17	53	20.9	450	2 S12099	hypothetical prote
18	53	20.9	765	2 S74598	hypothetical prote
19	53	20.9	860	2 UC5702	ERBB kinase activa
20	53	20.9	868	2 UC5701	ERBB kinase activa
21	52.5	20.7	347	2 P26349	hypothetical prote
22	52.5	20.7	910	2 AE3380	valine-tRNA ligase
23	52	20.5	381	2 S38663	hypothetical prote
24	52	20.5	665	2 C81439	probable integral
25	52	20.5	2870	2 H96974	cyclic beta 1-2 gl
26	52	20.5	3898	1 GNMVHB	genome polyprotein
27	52	20.5	3898	1 S57437	genome polyprotein
28	52	20.5	3898	2 S58295	polyprotein - hog
29	51.5	20.3	461	2 B95388	Probable (EC 1.1.1

30	51.5	20.3	977	2 I52657	seizure-related pr
31	51	20.1	106	2 A05148	hypothetical reduc
32	51	20.1	407	2 I52703	42k membrane glyco
33	51	20.1	552	2 S15555	NAD synthase (EC 6
34	51	20.1	771	2 G71409	probable replicati
35	51	20.1	813	2 E85135	hypothetical prote
36	51	20.1	1359	2 T10235	xanthine dehydroge
37	51	20.1	3898	1 GNMVHC	genome polyprotein
38	51	20.1	4544	1 S02392	alpha-2-macroglobu
39	50.5	19.9	296	2 T12469	hypothetical prote
40	50.5	19.9	317	2 S20287	peroxidase (EC 1.1
41	50.5	19.9	397	2 T19022	hypothetical prote
42	50.5	19.9	460	2 AG2262	hypothetical prote
43	50.5	19.9	488	2 T31622	hypothetical prote
44	50.5	19.9	503	2 A85900	hypothetical prote
45	50.5	19.9	503	2 E91055	hypothetical prote

#### ALIGNMENTS

RESULT 1  
JN0684  
adrenomedullin precursor - human  
C:Date: 03-Feb-1994 #sequence revision 03-Feb-1994 #text\_change 09-Jul-2004  
C:Accession: J02351; JN0684; E05548; JN0476  
R:Ichimaru, T.; Kojima, M.; Kangawa, K.; Hino, J.; Matsuo, H.; Kitamura, K.; Eto, T.;  
Biochem. Biophys. Res. Commun. 203, 631-639, 1994  
A:Title: Genomic structure of human adrenomedullin gene.  
A:Reference number: J02351; PMID:94354869; PMID:8074714  
A:Accession: J02351  
A:Molecule type: DNA  
A:Residues: 1-185 <185>  
A:Cross-references: UNIPROT:P35318; GB:S73906; NID:G765329; PID:AA06042.1; PID:G765330  
A:Experimental source: pheochromocytoma  
R:Kitamura, K.; Sakata, J.; Kangawa, K.; Kojima, M.; Matsuo, H.; Eto, T.  
Biochem. Biophys. Res. Commun. 194, 720-725, 1993  
A:Title: Cloning and characterization of cDNA encoding a precursor for human adrenomedullin.  
A:Reference number: JN0684; PMID:93343928; PMID:7688224  
A:Accession: JN0684  
A:Molecule type: mRNA  
A:Residues: 1-185 <185>  
A:Cross-references: GB:D14874; NID:G455470; PID:BA03589.1; PID:G500612  
A:Accession: E05548  
A:Molecule type: protein  
A:Residues: 22-41 <R12>  
R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Nakamura, S.; Matsuo, H.; Eto, T.  
Biochem. Biophys. Res. Commun. 192, 553-560, 1993  
A:Title: Adrenomedullin: A novel hypotensive peptide isolated from human pheochromocytoma  
A:Reference number: JN0476; PMID:93249425; PMID:8387282  
A:Accession: JN0476  
A:Molecule type: protein  
A:Residues: 95-146 <R13>  
A:Experimental source: pheochromocytoma  
C:Genetics:  
A:Gene: GDB:ADM  
A:Cross-references: GDB:217070; OMIM:103275  
A:Map position: 11pter-11pter  
A:Insertions: 33/2; 83/2  
C:Keywords: amidated carboxyl end; blood pressure control; hormone  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-185/Product: proadrenomedullin #status predicted <PEP>  
F:22-41/Domain: proadrenomedullin amino-terminal 20 peptide #status predicted <PAP>  
F:95-146/Product: adrenomedullin #status experimental <NMT>  
F:147-185/Domain: carboxyl-terminal propeptide #status predicted <CTP>  
F:41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following glyk  
F:110-115/Disulfide bonds: #status experimental  
F:146/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following glyk)

Query Match 28.5%; Score 72.5; DB 2; Length 185;  
Best Local Similarity 38.5%; Pred. No. 0.037;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVONLSHRLWQMGAPGRODSAPVDPSSPHSY 47  
 Db 109 GCRFGCTCTVQKLAHQIYQFT-DKDXDGNVAPRKRISIPQGY 146

## RESULT 2

adrenomedullin - pig  
 S41600  
 C/Species: Sus scrofa domestica (domestic pig)  
 C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S41600  
 R/Kitamura, K.; Kangawa, K.; Kojima, M.; Ichiki, Y.; Matsuo, H.; Eto, T.  
 FEBS Lett. 338, 306-310, 1994  
 A/Title: Complete amino acid sequence of porcine adrenomedullin and cloning of cDNA encod  
 A/Reference number: S41600; MUID:9413945; PMID:8043068  
 A/Accession: S41600  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-188 <KIT>  
 A/Cross-references: UNIPROT:P53366; GB:D14875; NID:g439721; PIDN:BA03590.1; PID:g496379

Query Match 27.8%; Score 70.5; DB 2; Length 188;  
 Best Local Similarity 38.5%; Pred. No. 0.069;  
 Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVONLSHRLWQMGAPGRODSAPVDPSSPHSY 47  
 Db 109 GCRFGCTCTVQKLAHQIYQFT-DKDXDGNVAPRKRISIPQGY 146

## RESULT 3

adrenomedullin precursor - rat  
 JN0766  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 09-Jul-2004  
 C/Accession: JN0766; P0610  
 R/Sakata, J.; Shimokubo, T.; Kitamura, K.; Nakamura, S.; Kangawa, K.; Matsuo, H.; Eto, T.  
 Biochem. Biophys. Res. Commun. 195, 921-927, 1993  
 A/Title: Molecular cloning and biological activities of rat adrenomedullin, a hypotensive  
 A/Reference number: JN0766; MUID:93384621; PMID:7690563  
 A/Accession: JN0766  
 A/Molecule type: mRNA  
 A/Residues: 1-185 <SAK>  
 A/Cross-references: UNIPROT:P43145  
 A/Accession: P0610  
 A/Molecule type: protein  
 A/Residues: 22-41 <SA2>  
 C/Comment: This precursor contains a unique 20-amino acid sequence designated proadrenom  
 esure control.  
 C/Keywords: amidated carboxyl end  
 F/1-21/Domain: signal sequence #status predicted <SIG>  
 F/22-185/Product: proadrenomedullin #status predicted <PEU>  
 F/22-41/Product: proadrenomedullin amino-terminal 20 peptide #status predicted <PAp>  
 F/94-143/Product: adrenomedullin #status predicted <MKT>  
 F/41/Modified site: amidated carboxyl end (Arg) (amide in mature form from following gly  
 F/143/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 27.4%; Score 69.5; DB 2; Length 185;  
 Best Local Similarity 35.9%; Pred. No. 0.092;  
 Matches 14; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCQVONLSHRLWQMGAPGRODSAPVDPSSPHSY 47  
 Db 106 GCRFGCTCTVQKLAHQIYQFT-DKDXDGNVAPRKRISIPQGY 143

## RESULT 4

AC3406  
 1-lactate permease [imported] - Brucella melitensis (strain 16M)  
 C/Species: Brucella melitensis  
 C/Date: 01-Feb-2002 #sequence\_revision 01-Feb-2002 #text\_change 09-Jul-2004  
 C/Accession: AC3406

R./delVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujter, C.; Los, T.; Ivanova, I.  
 ; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagler, S.; O'Callaghan, D.; Letesec  
 Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002  
 A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis  
 A/Reference number: AD3252; PMID:11756688  
 A/Accession: AC3406  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-339 <KUR>  
 A/Cross-references: UNIPROT:O8YGC6; GB:AE008917; PIDN:AAL52414.1; PID:g17983216; GSPDB:GR  
 A/Experimental source: strain 16M  
 C/Genetics:  
 A/Status: preliminary  
 A/Map position: I

Query Match 22.8%; Score 58; DB 2; Length 339;  
 Best Local Similarity 27.7%; Pred. No. 5.9;  
 Matches 13; Conservative 6; Mismatches 20; Indels 8; Gaps 1;

Qy 8 VCCVLGTCQVONLSHRLWQMGAPGRODSAPVDPSSPHS 46  
 Db 31 VDVIATCMAALAFRLFQPRRIWTSTGKEBTNAPVQPRSHS 77

## RESULT 5

alpha-1A adrenergic receptor - rat  
 A38731  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 22-Jan-1993 #sequence\_revision 22-Jan-1993 #text\_change 09-Jul-2004  
 C/Accession: A38731; A53280  
 R/Lomansney, J.W.; Cotecchia, S.; Lorenz, W.; Leung, W.Y.; Schwinn, D.A.; Yang-Feng, T.L.;  
 J. Biol. Chem. 266, 6365-6369, 1991  
 A/Title: Molecular cloning and expression of the cDNA for the alpha-1A-adrenergic recept  
 A/Reference number: A38731; MUID:91177889; PMID:1706716  
 A/Accession: A38731  
 A/Molecule type: mRNA  
 A/Residues: 1-560 <LOM>  
 A/Cross-references: UNIPROT:P23944; GB:M60654; NID:g202761; PIDN:AAA63477.1; PID:g202762  
 R/Perez, D.M.; Pisacit, M.T.; Graham, R.M.  
 Mol. Pharmacol. 40, 876-883, 1991  
 A/Title: Solution-phase library screening for the identification of rare clones: isolatic  
 A/Reference number: A53280; MUID:92100054; PMID:1661838  
 A/Accession: A53280  
 A/Status: preliminary; not compared with conceptual translation  
 A/Molecule type: mRNA  
 A/Residues: 1-36, 'P', 38-58, 'I', 60-202, 'I', 204-305, 'R', 307-366, 'I', 368-370, 'I', 372-559 <PE  
 A/Experimental source: hippocampus  
 A/Note: sequence extracted from NCBI backbone (NCBIP:73541)  
 C/Superfamily: vertebrate rhodopsin  
 C/Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein

Query Match 22.8%; Score 58; DB 2; Length 560;  
 Best Local Similarity 30.9%; Pred. No. 10;  
 Matches 17; Conservative 3; Mismatches 15; Indels 20; Gaps 2;

Qy 4 QLRVGVGTCQVONLSHRLWQMGAPGRODSAPVDPSSPH 45  
 Db 409 RLNR-----CQRRRRRLMSLRPLSLDRRRRLRPPSHSPKPPSSPH 456

## RESULT 6

T29482  
 hypothetical protein F08B4.2 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T29482  
 R/Stelljes, L.; Gattung, S.  
 submitted to the EMBL Data Library, March 1996  
 A/Description: The sequence of C. elegans cosmid F08B4.  
 A/Reference number: Z20625  
 A/Accession: T29482  
 A/Status: preliminary; translated from GB/EMBL/DDBJ  
 A/Molecule type: DNA

A;Residues: 1-1544 <STE>  
A;Cross-references: UNIPROT:Q019194; EMBL:U52002; PDB:AA837728.1; GSPDB:GN00022; CESP:FC  
A;Experimental source: strain Bristol N2; clone F08B4  
C;Genetics:  
A;Gene: CESP.F08B4.2  
A;Map position: 4  
A;Intons: 25/3; 74/3; 147/3; 238/1; 290/2; 391/2; 452/3; 526/3; 670/3; 734/1; 779/3; 83

Query Match 22.4%; Score 58; DB 2; Length 1544;  
Best Local Similarity 25.4%; Pred. No. 30;  
Matches 15; Conservative 7; Mismatches 23; Indels 14; Gaps 1;

QY 3 AQLRVGCVLTGTCOV-----ONTLSRLMQLMGPAGRODSAPVDPSSPSHY 47  
DB 1275 AVTVAGALIGICAVCFWGRYKTAQRNANSHSYQKGLPIYHPTMGVDPRTXYDY 1333

# RESULT 7

T02844  
cdc6-related protein, L3169.1 [imported] - Leishmania major (strain Friedlin)  
C;Species: Leishmania major  
C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 09-Jul-2004  
C;Accession: H81461; T02844

R;Wylet, P.J.; Audleman, L.; devos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.;  
Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999  
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-c  
A;Reference number: A81455; MUID:99178987; PMID:10077609  
A;Accession: H81461

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1784 <PVL>  
A;Cross-references: UNIPROT:Q94606; GB:AE001274; NID:G3264850; PDB:AA24667.1; PID:G326  
A;Experimental source: strain MHOM/IL/81/Friedlin  
C;Genetics:  
A;Gene: L3169.1  
A;Map position: 1

Query Match 22.4%; Score 57; DB 2; Length 1784;  
Best Local Similarity 52.6%; Pred. No. 47;  
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 16 QVONLSRLMQLMGPAGRO 34  
DB 321 ELQHLWHTLWELLGAAMRQ 339

# RESULT 8

E82662  
ABC transporter ATP-binding protein XF1602 [imported] - Xylella fastidiosa (strain 9a5c)  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: E82662

R;Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: A82515; MUID:20365717; PMID:10910347  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: E82662

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-283 <SIM>  
A;Cross-references: UNIPROT:Q9PD02; GB:AE003987; GB:AE003849; NID:G9106634; PDB:AAE8441  
A;Experimental source: strain 9a5c

R;Stimpson, A.U.G.; Reinech, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Carraro, D.M.; Carreir, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Faciniani, A.P.; Ferreira, A.J.S.  
submitted to Genbank, June 2000  
A;Authors: Ferreira, V.C.A.; Perro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitejima, J.P.; Krieger, J.E.; Kurame, E.B.; Laizy  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E  
A;Authors: Martins, E.M.F.; Matsushima, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshahko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF1602

Query Match 21.3%; Score 54; DB 2; Length 283;  
Best Local Similarity 34.1%; Pred. No. 17;  
Matches 15; Conservative 7; Mismatches 18; Indels 4; Gaps 1;

QY 1 TQAQLRVGCVLTGTCOVONLSRLMQLMGPAGRODSAPVDPSSPSHY 40  
DB 195 TDVAFIRDFGHLVINTDVONLSRLMQLMGPAGRODSAPVDPSSPSHY 238

# RESULT 9

T26050  
hypothetical protein W01C9.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T26050

R;Stims, M.  
submitted to the EMBL Data Library, June 1995  
A;Reference number: Z20143  
A;Accession: T26050  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-792 <WIL>  
A;Cross-references: UNIPROT:Q23115; EMBL:Z49969; PDB:CAA90267.1; GSPDB:GN00020; CESP:WO:  
A;Experimental source: clone W01C9  
C;Genetics:  
A;Gene: CESP.W01C9.3  
A;Map position: 2  
A;Intons: 15/1; 40/1; 66/3; 101/3; 182/2; 270/3; 338/3; 366/1; 597/3; 613/2; 646/2; 684,

Query Match 21.3%; Score 54; DB 2; Length 792;  
Best Local Similarity 39.5%; Pred. No. 50;  
Matches 15; Conservative 3; Mismatches 18; Indels 2; Gaps 1;

QY 9 GCVLGTCOVONLSRLMQLMGPAG--RQDSAPVDPSSP 44  
DB 736 GLALENRDADGFSHRLQQLMGTSNRYRDPVDPVNVNP 773

# RESULT 10

A43708  
gamma-interferon-inducible protein IP-30 precursor - human  
C;Species: Homo sapiens (man)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A43708

R;Luster, A.D.; Weinshank, R.L.; Feilman, R.; Ravetch, J.V.  
J. Biol. Chem. 263, 12036-12043, 1988  
A;Title: Molecular and biochemical characterization of a novel gamma-interferon-inducibl  
A;Reference number: A43708; MUID:88298888; PMID:3136170  
A;Accession: A43708

A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-303 <LUS>  
A;Cross-references: UNIPROT:P13284; EMBL:J03909; NID:G186264; PDB:AAA36105.1; PID:G30704

Query Match 21.1%; Score 53.5; DB 2; Length 303;  
Best Local Similarity 41.4%; Pred. No. 21;  
Matches 12; Conservative 3; Mismatches 11; Indels 3; Gaps 1;

QY 10 CVLGTGVONLSRLMQLMGPAGRODSAP 38  
DB 209 CSPATARVCAIGHRWETL---GRSDPAP 234

# RESULT 11

A37845  
carboxylesterase (EC 3.1.1.1) precursor - Streptomyces scabies

C:Species: Streptomyces scabies  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: A37845; PC1103  
R:Raymer, G.; Willard, J.M.A.; Schottel, J.L.  
J. Bacteriol. 172, 7020-7026, 1990  
A:Title: Cloning, sequencing, and regulation of expression of an extracellular esterase  
A:Reference number: A37845; MUID:91072254; PMID:2254271  
A:Accession: A37845  
A:Molecule type: DNA  
A:Residues: 1-345 <R>  
A:Cross-references: UNIPROT:P22266; GB:M57297; NID:g153254; PIDN:AAA26743.1; PID:g153255  
R:Schottel, J.L.; Hale, V.; Babcock, M.J.  
Gene 115, 27-31, 1992  
A:Title: Regulation and secretion of an extracellular esterase from Streptomyces scabies  
A:Reference number: PC1103; MUID:92307438; PMID:1612447  
A:Accession: PC1103  
A:Molecule type: DNA  
A:Residues: 1-54 <SCH>  
A:Cross-references: GB:M57297  
C:Comment: This protein is involved in suberin degradation.  
C:Genetics:  
A:Gene: est  
C:Keywords: carboxylic ester hydrolase  
F:1-33/Domains: signal sequence #status predicted <SIG>  
F:40-345/Product: carboxylesterase #status predicted <MAT>

Query Match 21.1%; Score 53.5; DB 2; Length 345;  
Best Local Similarity 34.2%; Pred. No. 24;  
Matches 13; Conservative 3; Mismatches 13; Indels 9; Gaps 1;

QY 4 QLRVGCVLGTCOVONLSHRLMQLMGPAGRODSAPVDP 41  
DB 16 RLTAALVAVLMSGLA-----LNGPAGSAGAPADP 44

RESULT 12  
T35335  
Hypothetical protein SCSH.19c - Streptomyces coelicolor  
C:Species: Streptomyces coelicolor  
C:Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 09-Jul-2004  
A:Accession: T35335  
R:Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, May 1999  
A:Reference number: Z21575  
A:Accession: T35335  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-136 <OLI>  
A:Cross-references: UNIPROT:Q9X767; EMBL:AL049863; PIDN:CAB42944.1; GSPDB:GN00070; SCOEI  
A:Experimental source: strain A3(2)  
C:Genetics:  
A:Gene: SCSH.19c

Query Match 20.9%; Score 53; DB 2; Length 136;  
Best Local Similarity 38.1%; Pred. No. 10;  
Matches 16; Conservative 3; Mismatches 19; Indels 4; Gaps 1;

QY 7 RRGCVLGTGVONLSHRLMQL-----MGPRGRODSAPVDPSSP 44  
DB 19 RIGVPLGTVPAPTLALMLWRDRAWIAERLDPPDTHLP 60

RESULT 13  
AE2414  
Hypothetical protein all4869 [imported] - Nostoc sp. (strain PCC 7120)  
C:Species: Nostoc sp. PCC 7120  
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C:Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C:Accession: AE2414  
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840  
A:Accession: AE2414  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-192 <KUR>  
A:Cross-references: UNIPROT:Q8VNR4; GB:BA000019; PIDN:BA076568.1; PID:g17134006; GSPDB:GN  
A:Experimental source: strain PCC 7120  
C:Genetics:  
A:Gene: all4869  
C:Superfamily: Synchocystis hypothetical protein str1160

Query Match 20.9%; Score 53; DB 2; Length 192;  
Best Local Similarity 40.0%; Pred. No. 15;  
Matches 8; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 27 LMGPAGRODSAPVDPSSPHS 46  
DB 23 LLAIVNAQNPPIDPNSPN 42

RESULT 14  
H95954  
probable Sir2-like transcription silencer protein [imported] - Sinorhizobium meliloti (str  
C:Species: Sinorhizobium meliloti  
C:Date: 24-Aug-2001 #sequence\_revision 24-Aug-2001 #text\_change 09-Jul-2004  
C:Accession: H95954  
R:Finan, T.M.; Weidner, S.; Wong, K.; Buhmester, J.; Chain, P.; Vorholter, F.J.; Hernan  
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001  
A:Title: The complete sequence of the 1,663-bp pSymB megaplasmid from the N2-fixing endo  
A:Reference number: A95842; MUID:21396508; PMID:11481431  
A:Accession: H95954  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-272 <KUR>  
A:Cross-references: UNIPROT:P96452; GB:AL591985; PIDN:CA9304.1; PID:g15140790; GSPDB:GN  
A:Experimental source: strain 1021, megaplasmid pSymB  
R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,  
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;  
L.; Hyman, R.W.; Jones, T.  
Science 293, 668-672, 2001  
A:Author: Kahn, D.; Kahn, M.L.; Kaiman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,  
habaut, P.; Vandendol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yen, K.C.  
A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.  
A:Reference number: A96039; MUID:21368234; PMID:11474104  
A:Contents: annotation  
C:Genetics:  
A:Gene: Smb21328  
A:Genome: plasmid  
C:Superfamily: uncharacterized conserved protein with Sir2 domain

Query Match 20.9%; Score 53; DB 2; Length 272;  
Best Local Similarity 26.1%; Pred. No. 22;  
Matches 12; Conservative 10; Mismatches 22; Indels 2; Gaps 1;

QY 2 QQLRVGCVLGTCOVONLSHRLMQLMGPAGRODSAPVDPSSPHSY 47  
DB 167 EATVPLGTGMSDNLIRLLIRWISIMRSGHEKDRP--PQVPMY 230

RESULT 15  
E97187  
dUDP-D-glucose 4,6-dehydratase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: E97187  
R:Noelling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,  
J.; Daly, M.J.; Bennett, G.N.; Kocun, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: E97187  
A:Status: preliminary  
A:Molecule type: DNA



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 4, 2005, 18:06:10 ; Search time 41 Seconds  
(without alignments)  
85.573 Million cell updates/sec

Title: US-10-723-368-5

Perfect score: 254  
Sequence: 1 TQQLRVGCVLTGTCVQYNL.....MGPRGRDSAPVDPSSPHSY 47

Scoring table: BIOSIM62

Gapop 10.0 , Gapept 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/1aa/PTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	72.5	28.5	38	4	US-09-280-501-6 Sequence 6, Appl
2	72.5	28.5	40	4	US-09-280-501-11 Sequence 11, Appl
3	72.5	28.5	52	3	US-09-070-504-14 Sequence 14, Appl
4	72.5	28.5	52	4	US-09-813-345C-14 Sequence 14, Appl
5	72.5	28.5	185	1	US-08-233-389C-1 Sequence 1, Appl
6	72.5	28.5	185	2	US-08-801-863-1 Sequence 1, Appl
7	72.5	28.5	185	2	US-08-486-596A-1 Sequence 1, Appl
8	72.5	28.5	185	2	US-09-004-713-1 Sequence 1, Appl
9	70.5	27.8	188	1	US-08-233-389C-3 Sequence 3, Appl
10	70.5	27.8	188	2	US-08-801-863-3 Sequence 3, Appl
11	70.5	27.8	188	2	US-08-486-596A-3 Sequence 3, Appl
12	70.5	27.8	188	2	US-09-004-713-3 Sequence 3, Appl
13	69.5	27.4	50	3	US-09-070-504-15 Sequence 15, Appl
14	69.5	27.4	40	4	US-09-813-345C-15 Sequence 15, Appl
15	65.5	25.8	50	4	US-09-280-501-8 Sequence 8, Appl
16	65.5	25.8	50	4	US-09-280-501-7 Sequence 7, Appl
17	58	22.8	559	2	US-08-406-855A-20 Sequence 20, Appl
18	58	22.8	559	3	US-09-206-899-20 Sequence 20, Appl
19	58	22.8	560	4	US-09-688-415-8 Sequence 8, Appl
20	56	22.0	172	4	US-09-949-016-9374 Sequence 9374, Ap
21	55	22.0	770	4	US-09-252-991A-28510 Sequence 28510, A
22	55.5	21.9	906	4	US-09-252-991A-22132 Sequence 22132, A
23	54.5	21.5	184	4	US-09-252-991A-32339 Sequence 32339, A
24	54	21.3	133	4	US-09-252-991A-30594 Sequence 30594, A
25	53.5	21.1	218	4	US-09-270-767-43455 Sequence 43455, A
26	53.5	21.1	303	4	US-09-949-016-6717 Sequence 6717, Ap
27	53	20.9	181	4	US-09-530-685A-21 Sequence 21, Appl

28	53	20.9	239	4	US-09-530-685A-32 Sequence 32, Appl
29	53	20.9	255	4	US-09-902-540-14178 Sequence 14178, A
30	53	20.9	309	4	US-09-530-685A-31 Sequence 31, Appl
31	53	20.9	450	3	US-09-120-365-68 Sequence 68, Appl
32	53	20.9	450	3	US-09-515-039-68 Sequence 68, Appl
33	53	20.9	605	3	US-08-753-007A-2 Sequence 2, Appl
34	53	20.9	605	3	US-09-398-496-2 Sequence 2, Appl
35	53	20.9	754	2	US-08-525-864A-2 Sequence 2, Appl
36	52	20.5	263	4	US-09-270-767-46206 Sequence 46206, A
37	52	20.5	675	4	US-09-252-991A-32681 Sequence 32681, A
38	52	20.5	3898	3	US-08-750-717-2 Sequence 2, Appl
39	51.5	20.3	149	4	US-09-543-681A-8072 Sequence 8072, Ap
40	51.5	20.3	155	4	US-09-252-991A-20281 Sequence 20281, A
41	51.5	20.3	220	4	US-09-902-540-11202 Sequence 11202, A
42	51.5	20.3	879	4	US-09-252-991A-31990 Sequence 31990, A
43	51	20.1	1213	2	US-08-937-102-2 Sequence 2, Appl
44	51	20.1	1399	4	US-09-388-221B-4 Sequence 4, Appl
45	51	20.1	1424	4	US-09-388-221B-12 Sequence 12, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-280-501-6
Sequence 6, Application US/09280501
Patent No. 6440421
GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: US/09/280,501
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 38
TYPE: PRT
ORGANISM: Homo sapiens
US-09-280-501-6

Query Match      28.5%; Score 72.5; DB 4; Length 38;
Best Local Similarity 38.5%; Pred. No. 0.0098;
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Cy      9 GCVLTGTCVQYNLSHRLMQLMGPRGRDSAPVDPSSPHSY 47
Db      1 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISPGY 38

RESULT 2
US-09-280-501-11
Sequence 11, Application US/09280501
Patent No. 6440421
GENERAL INFORMATION:
APPLICANT: Cooper, Garth James Smith
APPLICANT: Reid, Ian Reginald
APPLICANT: Cornish, Jillian
TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH
ADRENOMEDULLIN OR ADRENOMEDULLIN AGONISTS
FILE REFERENCE: 08987-005001
CURRENT APPLICATION NUMBER: US/09/280,501
PRIOR FILING DATE: 1999-03-30
PRIOR APPLICATION NUMBER: 08/634,562
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
```

LENGTH: 40  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-280-501-11

Query Match 28.5%; Score 72.5; DB 4; Length 40;  
Best Local Similarity 38.5%; Pred. No. 0.01;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAGRDSDAPVDPSSPHSY 47  
DB 3 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISFQGY 40

RESULT 3  
US-09-070-504-14

Sequence 14, Application US/09070504

Patent No. 6268474

GENERAL INFORMATION:

APPLICANT: Smith, Derek D.

APPLICANT: Saha, Shankar

APPLICANT: Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF GCRP-RECEPTOR

TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Muehling, Raasch & Gebhardt, P.A.

STREET: 119 No. 6268474th Fourth Street

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,504

FILING DATE: 30-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H

REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 52 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-070-504-14

Query Match 28.5%; Score 72.5; DB 3; Length 52;

Best Local Similarity 38.5%; Pred. No. 0.014;

Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAGRDSDAPVDPSSPHSY 47

DB 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISFQGY 52

RESULT 4  
US-09-813-345C-14

Sequence 14, Application US/09813345C

Patent No. 6756205

GENERAL INFORMATION:

APPLICANT: CREIGHTON UNIVERSITY

APPLICANT: SMITH, Derek D.

Query Match 28.5%; Score 72.5; DB 3; Length 52;

Best Local Similarity 38.5%; Pred. No. 0.014;

Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAGRDSDAPVDPSSPHSY 47

DB 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISFQGY 52

APPLICANT: SAHA, Shankar  
APPLICANT: ABEL, Peter W.  
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF GCRP-RECEPTOR SUPERFAMILY AND METHODS OF  
TITLE OF INVENTION: USE  
FILE REFERENCE: 180.00020102  
CURRENT APPLICATION NUMBER: US/09/813,345C  
CURRENT FILING DATE: 2001-03-20  
PRIOR APPLICATION NUMBER: 09/070,504  
PRIOR FILING DATE: 1998-04-30  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: Patent version 3.2  
SEQ ID NO 14  
LENGTH: 52

QY 9 GCVLGTQVONLSHRLMQLMGPAGRDSDAPVDPSSPHSY 47  
DB 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISFQGY 52

RESULT 5  
US-08-233-389C-1

Sequence 1, Application US/08233389C

Patent No. 5639855

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUDO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/O FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,389C

FILING DATE: 26-APR-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-233-389C-1

Query Match 28.5%; Score 72.5; DB 1; Length 185;

Best Local Similarity 38.5%; Pred. No. 0.056;

Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAGRDSDAPVDPSSPHSY 47

DB 15 GCRFGTCTVQKLAHQIYQFT-DKDKDNVAPRSKISFQGY 52



Qy 9 GCVLGTQOVONLSHRLWLMGPAGRODSAPVDPSPSHSY 47  
Db 109 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRSKISPGCY 146

## RESULT 6

US-08-801-863-1  
Sequence 1, Application US/08801863

Patent No. 5830703

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: c/o FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,863

FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5 DIV3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-801-863-1

Query Match 28.5%; Score 72.5; DB 2; Length 185;  
Best Local Similarity 38.5%; Pred. No. 0.056; Indels 1; Gaps 1;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

## RESULT 7

US-08-486-596A-1  
Sequence 1, Application US/08486596A

Patent No. 5837823

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: c/o FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,596A  
FILING DATE: JUNE 7, 1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HALEY Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-5 DIV1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 596-9000  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 185 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-486-596A-1

Query Match 28.5%; Score 72.5; DB 2; Length 185;  
Best Local Similarity 38.5%; Pred. No. 0.056; Indels 1; Gaps 1;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTQOVONLSHRLWLMGPAGRODSAPVDPSPSHSY 47  
Db 109 GCRFGTCTVQKLAHQIYQFT-DKDKXNVAPRSKISPGCY 146

RESULT 8  
US-09-004-713-1  
Sequence 1, Application US/09004713

Patent No. 5910416

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: c/o FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/004,713

FILING DATE: JANUARY 7, 1998

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: HALEY Jr., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 185 amino acids

TYPE: amino acid

Thu May 5 18:51:37 2005

us-10-723-368-5.fai

TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-004-713-1

Query Match  
Best Local Similarity 28.5%; Score 72.5; DB 2; Length 185;  
Matches 15; Conservative 6; Mismatches 17; Indels 1; Gaps 1;

Qy 9 GCVLGTCOVONLSHRLMQLMGPAGRODSAPVDPSSPHSY 47  
Db 109 GCRFGCTVOKLAHQIYQFT-DKDKDGVAPRSKISPOGY 146

RESULT 9

US-08-233-389C-3  
Sequence 3, Application US/08233389C  
Patent No. 5639655  
GENERAL INFORMATION:  
APPLICANT: KITAMURA, Kazuo  
APPLICANT: KANGAWA, Kenji  
APPLICANT: MATSUO, Hisayuki  
TITLE OF INVENTION: ADRENOMEDULLIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/233.389C  
FILING DATE: 26-APR-1994  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HALEY Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-5  
TELEPHONE: (212) 596-9090  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-233-389C-3

Query Match  
Best Local Similarity 27.8%; Score 70.5; DB 1; Length 188;  
Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

Qy 9 GCVLGTCOVONLSHRLMQLMGPAGRODSAPVDPSSPHSY 47  
Db 109 GCRFGCTVOKLAHQIYQFT-DKDKDGVAPRSKISPOGY 146

RESULT 10  
US-08-801-863-3  
Sequence 3, Application US/08801863  
Patent No. 5830703  
GENERAL INFORMATION:  
APPLICANT: KITAMURA, Kazuo  
APPLICANT: KANGAWA, Kenji  
APPLICANT: MATSUO, Hisayuki  
APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/801.863  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HALEY Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-5 DIV3  
TELEPHONE: (212) 596-9090  
TELEFAX: (212) 596-9090  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 188 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-801-863-3

Query Match  
Best Local Similarity 27.8%; Score 70.5; DB 2; Length 188;  
Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

Qy 9 GCVLGTCOVONLSHRLMQLMGPAGRODSAPVDPSSPHSY 47  
Db 109 GCRFGCTVOKLAHQIYQFT-DKDKDGVAPRSKISPOGY 146

RESULT 11  
US-08-486-596A-3  
Sequence 3, Application US/08486596A  
Patent No. 5837823  
GENERAL INFORMATION:  
APPLICANT: KITAMURA, Kazuo  
APPLICANT: KANGAWA, Kenji  
APPLICANT: MATSUO, Hisayuki  
TITLE OF INVENTION: ADRENOMEDULLIN  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: C/O FISH & NEAVE  
STREET: 1251 Avenue of the Americas  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10020  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486.596A  
FILING DATE: JUNE 7, 1995  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: HALEY Jr., James F.  
REGISTRATION NUMBER: 27,794  
REFERENCE/DOCKET NUMBER: SHGN-5 DIV1

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 188 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-486-596A-3

Query Match 27.8%; Score 70.5; DB 2; Length 188;  
 Best Local Similarity 38.5%; Pred. No. 0.11;  
 Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAQRDSAPVDPSSPHSY 47  
 DB 109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPGGY 146

RESULT 12  
 US-09-004-713-3  
 Sequence 3, Application US/09004713  
 Patent No. 5910416  
 GENERAL INFORMATION:  
 APPLICANT: KITAMURA, Kazuo  
 APPLICANT: KANAGAWA, Kenji  
 APPLICANT: MATSUO, Hisayuki  
 APPLICANT: ETO, Tanemao  
 TITLE OF INVENTION: ADRENOMEDULLIN  
 NUMBER OF SEQUENCES: 10  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: C/O FISH & NEAVE  
 STREET: 1251 Avenue of the Americas  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10020  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/004,713  
 FILING DATE: JANUARY 7, 1998  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: HALEY JR., James F.  
 REGISTRATION NUMBER: 27,794  
 REFERENCE/DOCKET NUMBER: SHGN-5 DIV2 CON  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 596-9000  
 TELEFAX: (212) 596-9090  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 188 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-004-713-3

Query Match 27.8%; Score 70.5; DB 2; Length 188;  
 Best Local Similarity 38.5%; Pred. No. 0.11;  
 Matches 15; Conservative 5; Mismatches 18; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAQRDSAPVDPSSPHSY 47  
 DB 109 GCRFGTCTVQKLAHQIYQFT-DKDKDGVAPRSKISPGGY 146

RESULT 13  
 US-09-070-504-15

Sequence 15, Application US/09070504  
 Patent No. 6268474  
 GENERAL INFORMATION:  
 APPLICANT: Smith, Derek D.  
 APPLICANT: Saha, Shankar  
 APPLICANT: Abel, Peter W.  
 TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR  
 TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Mueling, Raasch & Gebhardt, P.A.  
 STREET: 119 No. 6268474th Fourth Street  
 CITY: Minneapolis  
 STATE: MN  
 COUNTRY: USA  
 ZIP: 55401  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/070,504  
 FILING DATE: 30-Apr-1998  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McCormack, Myra H  
 REGISTRATION NUMBER: 36,602  
 REFERENCE/DOCKET NUMBER: 180.00020101  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612/305-1220  
 TELEFAX: 612/305-1228  
 INFORMATION FOR SEQ ID NO: 15:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 50 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-070-504-15

Query Match 27.4%; Score 69.5; DB 3; Length 50;  
 Best Local Similarity 35.9%; Pred. No. 0.033;  
 Matches 14; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTQVONLSHRLMQLMGPAQRDSAPVDPSSPHSY 47  
 DB 13 GCRFGTCTVQKLAHQIYQFT-DKDKDGMAPRNKISPGGY 50

RESULT 14  
 US-09-813-345C-15  
 Sequence 15, Application US/09813345C  
 Patent No. 6756205  
 GENERAL INFORMATION:  
 APPLICANT: CREIGHTON UNIVERSITY  
 APPLICANT: SMITH, Derek D.  
 APPLICANT: SAHA, Shankar  
 APPLICANT: ABEL, Peter W.  
 TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR SUPERFAMILY AND METHODS OF  
 TITLE OF INVENTION: USE  
 FILE REFERENCE: 180.00020102  
 CURRENT APPLICATION NUMBER: US/09/813,345C  
 CURRENT FILING DATE: 2001-03-20  
 PRIOR APPLICATION NUMBER: 09/070,504  
 PRIOR FILING DATE: 1998-04-30  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 SEQ ID NO 15  
 LENGTH: 50  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:

OTHER INFORMATION: Artificially Synthesized Peptide  
US-09-813-345C-15

Query Match 27.4%; Score 69.5; DB 4; Length 50;  
Best Local Similarity 35.9%; Pred. No. 0.033;  
Matches 14; Conservative 7; Mismatches 17; Indels 1; Gaps 1;

QY 9 GCVLGTCOVONLSHRLMOLMGPAQRDSAPVDPSSPHSY 47  
DB 13 GCRFGCTVQKLAHQIYQFT-DKDKDMAPRNKISPGY 50

RESULT 15

US-09-280-501-8  
; Sequence 8; Application US/09280501  
; Patent No. 6440421  
; GENERAL INFORMATION:  
; APPLICANT: Cooper, Garth James Smith  
; APPLICANT: Reid, Ian Reginald  
; APPLICANT: Cornish, Jillian  
; TITLE OF INVENTION: TREATMENT OF BONE DISORDERS WITH  
; FILE REFERENCE: 08987-005001  
; CURRENT FILING DATE: 1999-03-30  
; PRIOR APPLICATION NUMBER: 08/634,562  
; PRIOR FILING DATE: 1996-04-18  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 40  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-280-501-8

Query Match 25.8%; Score 65.5; DB 4; Length 40;  
Best Local Similarity 38.9%; Pred. No. 0.089;  
Matches 14; Conservative 6; Mismatches 15; Indels 1; Gaps 1;

QY 9 GCVLGTCOVONLSHRLMOLMGPAQRDSAPVDPSSP 44  
DB 5 GCRFGCTVQKLAHQIYQFT-DKDKDMAPRNKISP 39

Search completed: May 4, 2005, 18:15:51  
Job time : 50 secs